

STIC-Biotech/ChemLib

161646

My

From: Hamud, Fozia
Sent: Thursday, August 04, 2005 4:29 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/717,282

Please search 10/717,282, SEQ ID NO: 2 full length and residues 36-753; SEQ ID NO:1 full length and 86-234 against commercial data bases. thanks

Fozia Hamud
Patent Examiner
Remsen 4D64
Mail Box: Remsen 4C70
(571) 272-0884
Art Unit 1647

STIC-Biotech/ChemLib
10/717,282
10/717,282

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Searcher: _____
Searcher Phone: 2- _____
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Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2005, 22:16:13 ; Search time 10621.6 Seconds
(without alignments)
10871.157 Million cell updates/sec

Title: US-10-717-282-1
Perfect score: 2383
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:★

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2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sta:
12: gb_sy:
13: gb_un:
14: gb_vi:

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
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2	2376.6	99.7	2383	6	AX364573	AX364573	Sequence
3	2289	96.1	2341	9	AX364576	AX364576	Sequence
4	2282.6	95.8	4477	9	AF494208	AF494208	Homo sapi
5	2218.6	93.1	2786	6	AX350979	AX350979	Sequence
6	2215.4	93.0	3083	6	AX251723	AX251723	Sequence
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RESULT 4
AF494208
LOCUS AF494208 4477 bp mRNA linear PRI 08-DEC-2003
DEFINITION Homo sapiens interleukin 17 receptor-like protein long form
(IL17RLM) mRNA, complete cds; alternatively spliced.
ACCESSION AF494208

VERSION	AF494208.1	GI:21667503	
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AUTHORS	Xiong, S., Zhao, Q., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S., Liu, L., and Chang, Z.		
TITLE	hSef inhibits PC-12 Cell Differentiation by Interfering with Ras-Mitogen-activated Protein Kinase MAPK Signaling		
JOURNAL	J. Biol. Chem. 278 (50), 50273-50282 (2003)		
PUBMED	12958313		
REFERENCE	2 (bases 1 to 4477)		
AUTHORS	Xiong, S. Q., Huang, G. R., Zhao, Q. H., Chen, P. L., Rong, Z. L., Ye, X. Y., Chen, Y., Liu, L., Fu, X. Y. and Chang, Z. J.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-MAR-2002) Tsinghua Institute of Genome Research, Department of Biological Sciences and Biotechnology, and School of Medicine, Tsinghua University, Beijing 100084, P.R. China		
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ORIGIN			
Query Match	95.8%; Score 2282.6; DB 9; Length 4477;		
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AUTHORS	Gorman, D.M.				
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DB	1766	TCCATCTCTCCACTCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGG	1825
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RESULT. T 6

AX251723

LOCUS

DEFINITI

ACCESSION

VERSION

KEYWORDS
SOURCE

SOURCE
ORGAN

TATUOYO

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WO0168859.

Arthropoda; Craniata; Vertebrata; Euteleostomi;

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VERSION AF458067.1 GI:21779862
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2724)
AUTHORS Gilbert,J.M. and Gorman,D.M.
TITLE Identification of novel IL-17 related receptors
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2724)
AUTHORS Gilbert,J.M. and Gorman,D.M.
TITLE Direct Submission
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California Ave., Palo Alto, CA 94304, USA
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DEFINITION Sequence 15 from Patent WO0214358.
ACCESSION AX392973
VERSION AX392973.1 GI:19701020
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Edmonds,B.T., Micanovic,R., Ou,W., Su,E.W., Tschang,S.H. and Wang,H.
AUTHORS Novel secreted proteins and their uses
TITLE Patent: WO 0214358-A 15 21-FEB-2002;
JOURNAL ELI LILLY AND COMPANY (US)
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ACCESSION AX747904.1 GI:32132292
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
Masuho, Y.
Full-length cDNA sequences
Patent: EP 1308459-A 1429 07-MAY-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)
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ACCESSION AK093074			
VERSION AK093074.1 GI:21751823			
KEYWORDS oligo capping; fis (full insert sequence).			
SOURCE Homo sapiens			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS			
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Iehii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yaeuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoaka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,			
Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Teraohima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yanada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.			
Complete sequencing and characterization of 21,243 full-length human cDNAs			
Nat. Genet. 36 (1), 40-45 (2004)			
14702039			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Iehii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.			
NEDO human cDNA sequencing project			
Unpublished			
3 (bases 1 to 2894)			
Isogai, T. and Yamamoto, J.			
Direct Submission			
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan			
(E-mail: genomics@hri.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986)			
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.			
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RESULT 11

AF494211

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

AF494211 4478 bp mRNA linear PRI 08-DEC-2003
Homo sapiens interleukin 17 receptor-like protein short form
(IL17RLM) mRNA, complete cds; alternatively spliced.
AF494211
AF494211.1 GI:21667509

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1. (bases 1 to 4478)
AUTHORS	Xiong,S., Zhao,Q., Rong,Z., Huang,G., Huang,Y., Chen,P., Zhang,S., Liu,L. and Chang,Z.
TITLE	hSef Inhibits PC-12 Cell Differentiation by Interfering with Ras-Mitogen-activated Protein Kinase MAPK Signaling
JOURNAL	J. Biol. Chem. 278 (50), 50273-50282 (2003)
PUBMED	12958313
REFERENCE	2. (bases 1 to 4478)
AUTHORS	Xiong,S., Zhao,Q., Huang,G., Chen,P., Rong,Z., Ye,X., Chen,Y., Liu,L., Fu,X. and Chang,Z.
TITLE	Direct Submission
JOURNAL	Submitted (22-MAR-2002) Tsinghua Institute of Genome Research, Department of Biological Sciences and Biotechnology, and School of Medicine, Tsinghua University, Beijing 100084, P.R. China
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1			
Wiemann, S.			
Human dna sequences			
Patent: WO 0112659-A 616 22-FEB-2001;			
German Human Genome Project (DE)			

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VERSION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2406)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gaassenhuber,J. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2002) GSF, Institut fuer Bioinformatik MIPS, Ingolstaedter Landstr. 1, 85764 Neuherberg, Germany
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kiz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFp434L0320) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.

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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Kzyvinski,M.I., Skalska,U., Smalius,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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2 (bases 1 to 4490)
Strausberg,R.
Direct Submission
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgbcm.tmc.edu
Günaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,
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A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
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Qy	1828	CCATCTCTCCACTCGCTACCGGAGCGAGTCTTGGAGAAATTTGATTCGGGCTTGT	1887
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LOCUS			
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ACCESSION	AY489047		
VERSION	AY489047.1 GI:42411054		
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Altuvia, Y. and Ron, D.		
TITLE	Alternative splicing generates an isoform of the human SeF gene with altered subcellular localization and specificity		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 101 (5), 1229-1234 (2004)		
PUBMED	14742870		
REFERENCE	2 (bases 1 to 2364)		
AUTHORS	Ron, D.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-NOV-2003) Biology, Technion, Israel Institute of Technology, Haifa 32000, Israel		
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Qy	748	CAGCCAGCATGGCTCGGACATGCAAGTGTCTCTTCGACCATGCACCGCACAACTTCGCGCTT	807
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Qy	1108	AAATATATATTTACATTTAGATGAAGAGACTCTGAGTCTTCCACATPACACTCGACACT	1167
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Qy	1168	CCCAAGAGAGAGGCTCCGGCGCGGCGCGGAAGGTTCTTCTGCTATTTCAGTAAAGATGG	1227
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Qy	1228	CCAGAAATCATAAGTAATGTGCTCAGTGTTCGCCCTACTTCTCAGAGACTTCTGTGGCTG	1287
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us-10-717-282-1.rge

Sat Aug 13 10:40:49 2005

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2005, 19:37:18 ; Search time 1348.1 Seconds
(without alignments)
10464.155 Million cell updates/sec

Title: US-10-717-282-1

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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2289	96.1	2341	6	ABA95035 Human cyt
4	2218.6	93.1	2786	6	AA518134 Human DNA
5	2215.4	93.0	3083	4	AA515346 DNA encod
6	2158.4	90.6	4392	6	ABK62082 Human cDN
7	2128	89.3	2894	10	ADB63275 Human cDN
8	2127.2	89.3	2406	5	ABX71363 Human tra
9	2074.2	87.0	2319	4	AA509517 Human cDN
10	2074.2	87.0	2319	8	ACA89858 Human cDN
11	2074.2	87.0	2319	8	ACA64642 Human cDN
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13	2074.2	87.0	2319	9	ADA49781 Human int
14	2074.2	87.0	2319	9	ADA26974 cDNA enco
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17	2074.2	87.0	2319	10	ADG87392 Human PRO
18	2074.2	87.0	2319	10	ADL16688 cDNA enco
19	2074.2	87.0	2319	12	ADL16649 cDNA enco
20	2074.2	87.0	2319	12	ADL71309 Human IL-

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31	393.2	16.5	453	9	ACH39213 Human foe
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ALIGNMENTS

RESULT 1

ABA95031
ID ABA95031 standard; DNA; 2383 BP.

AC ABA95031;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 nucleotide sequence.

KW Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
pulmonary alveolar proteinosis; familial periodic fever; antitumor;
erythroleukemia; chromosome 3p14.3; gene therapy; ds.

OS Homo sapiens.

FH Key Location/Qualifiers
CDS 86..2347

FT /*tag= a

FT /product= "Zcytor18"

PN WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

PR 26-JUL-2000; 2000US-0220747P.

PA (ZYMO) ZYMOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

DR WPI; 2002-217048/27.

DR P-PSDB; ABB07626.

PT New cytokine receptor polypeptide designated zcytor18, useful for
inhibiting cell proliferation associated with psoriasis or tumor growth,
and modulating immune system by binding to endogenous zcytor18 ligand.

PS Claim 5; Page 85-90; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide

CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 nucleotide sequence
XX

SQ Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 U; 0 Other;

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Db 181	CGCGCGCGCGCGCGACACTGTGGCTGGAGGATGAAGCGGCTGCCGACCCCGGCTTTG	240		
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Db 781	CGACCATGCACCGCAACCTTCGGCTTCGGTTCCTTCTATCTTCACTACAAGCTCAAGCA	840
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Db 841	CGAAGGACCTTTTCAAGGAAAGACCTCTAAGCAGGAGCAAACTACAGAGAGCAGCAGCTG	900
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Qy 1861	CTTGAGAAAATTTGATTCGGGCTTGGTTTAAATGATGTCTATGTGCAACACGAGGCTTGA	1920
Db 1861	CTTGAGAAAATTTGATTCGGGCTTGGTTTAAATGATGTCTATGTGCAACACGAGGCTTGA	1920

DR WPI; 2002-217048/27.
XX P-PSDB; ABB07628.
PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
PS Claim 5; Page 102-106; 119pp; English.
XX
XX The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 splice variant nucleotide sequence
XX
SQ Sequence 2341 BP; 550 A; 668 C; 625 G; 498 T; 0 U; 0 Other;
Query Match 96.1%; Score 2289; DB 6; Length 2341;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2341; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
QY 1 CGCGCGCGCCACCGCCCACTCGGGGCTGGCCAGCGGGCGGGCGGGCGGCGAGAAC 60
DB 1 CGCGCGCGCCACCGCCCACTCGGGGCTGGCCAGCGGGCGGGCGGGCGGCGAGAAC 60
QY 61 GCGCTGGCTGGCGGAGCGGCAATGGCCCGGCTGGCTGGAGCTCTGCTCGCTTCTT 120
DB 61 GCGCTGGCTGGCGGAGCGGCAATGGCCCGGCTGGCTGGAGCTCTGCTCGCTTCTT 120
QY 121 TACGGTCAACGCTCGCTCAACGGCTCGCAGCTGGCTGGCGGCTGGCGGCTGGCGGCG 180
DB 121 TACGGTCAACGCTCGCTCAACGGCTCGCAGCTGGCTGGCGGCTGGCGGCTGGCGGCG 180
QY 181 CGCGCGGGCGCGGACACCTGTGGCTGGAGGATGAAGCGGCTGCCCGACCCCGGCTTTG 240
DB 181 CGCGCGGGCGCGGACACCTGTGGCTGGAG----- 210
QY 241 TGTGCTAATGAGGAGTGGGCGCCAGCGAGAACAGTGGGCTGTACACATCACCTT 300
DB 211 -----GGGAGTGGGCGCCAGCCAGAGAACAGTGGGCTGTACACATCACCTT 258
QY 301 CAATATGACAAATGACCACTTACCACTTGAATCCAGTGGGAGCATGTGATTGCTGACGC 360
DB 259 CAATATGACAAATGACCACTTACCACTTGAATCCAGTGGGAGCATGTGATTGCTGACGC 318
QY 361 CCAGAAATACCAATCAGCCAGTATGCTTGCATGACCAAGTGGCAGTCAACATTTCTTTG 420
DB 319 CCAGAAATACCAATCAGCCAGTATGCTTGCATGACCAAGTGGCAGTCAACATTTCTTTG 378
QY 421 GTCCCGAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTAACTCTGAGAGCT 480
DB 379 GTCCCGAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTAACTCTGAGAGCT 438
QY 481 GAGTCCGGGAGGAGCAGTGCACAACTGATTTCTAAGGATCCGAGCAGCTCAACAG 540
DB 439 GAGTCCGGGAGGAGCAGTGCACAACTGATTTCTAAGGATCCGAGCAGCTCAACAG 498
QY 541 TAGCTTCAAAAGAACTGGAAATGGAATCTCAACCTTTCTTGAATATGAATTTGAAACGGA 600
DB 499 TAGCTTCAAAAGAACTGGAAATGGAATCTCAACCTTTCTTGAATATGAATTTGAAACGGA 558
QY 601 TTATTTTCGTAAGGTTGTCCTTTTCTTTTCAATTAATAAAGCAATTTACACCTTT 660
DB 559 TTATTTTCGTAAGGTTGTCCTTTTCTTTTCAATTAATAAAGCAATTTACACCTTT 618

QY 661 CTTCTTTAGAACCCGAGCCTGTGACCTGTGTGTTTACAGCCGAGCAATCTAGCTTTGTAACC 720
DB 619 CTTCTTTAGAACCCGAGCCTGTGACCTGTGTGTTTACAGCCGAGCAATCTAGCTTTGTAACC 678
QY 721 CTTCTGGAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGACGAGTGTCTT 780
DB 679 CTTCTGGAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGACGAGTGTCTT 738
QY 781 CGACATGACCGGACAACTTCCGCTTCCGTTTCTTCTATCTTCACTCAAGCTCAAGCA 840
DB 739 CGACATGACCGGACAACTTCCGCTTCCGTTTCTTCTATCTTCACTCAAGCTCAAGCA 798
QY 841 CGAAGGACCTTTTCAAGCGAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACAGCTG 900
DB 799 CGAAGGACCTTTTCAAGCGAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACAGCTG 858
QY 901 CTTCTTCAAAATGTTTCTCAGGGATATATATTAATGAGCTGGTGGATGACACTAACAC 960
DB 859 CTTCTTCAAAATGTTTCTCAGGGATATATATTAATGAGCTGGTGGATGACACTAACAC 918
QY 961 AACAGAAAGTGAATGATTAATGCTTAAAGCCAGTCACTCCCGTGGCGGGCCCAT 1020
DB 919 AACAGAAAGTGAATGATTAATGCTTAAAGCCAGTCACTCCCGTGGCGGGCCCAT 978
QY 1021 CAGAGCCGTGGCCCATCACAGTGCCACTGTGTAGTCAATTCGGCAATTCGGCAAGCTCTTCA 1080
DB 979 CAGAGCCGTGGCCCATCACAGTGCCACTGTGTAGTCAATTCGGCAATTCGGCAAGCTCTTCA 1038
QY 1081 TGTGATGTCGCGAAGAAAGCAAAAGAAATATATATTTACATTTAGATGAAGAGCTC 1140
DB 1039 TGTGATGTCGCGAAGAAAGCAAAAGAAATATATATTTACATTTAGATGAAGAGCTC 1098
QY 1141 TGAGTCTTCCACATACCTGCAGCACTCCCAAGAGAGAGGCTCCGGCGCGGCCAAGGT 1200
DB 1099 TGAGTCTTCCACATACCTGCAGCACTCCCAAGAGAGAGGCTCCGGCGCGGCCAAGGT 1158
QY 1201 CTTTCTCTGTATTTCCAGTAAAGATGGCCAGAATCACAATGATGTGTCGATGTTTCCG 1260
DB 1159 CTTTCTCTGTATTTCCAGTAAAGATGGCCAGAATCACAATGATGTGTCGATGTTTCCG 1218
QY 1261 CTACTTCTCAGAGCTTCTGTGGCTGTGAGTGGCTCTGGAACCTGTGGGAAGACTTCAG 1320
DB 1219 CTACTTCTCAGAGCTTCTGTGGCTGTGAGTGGCTCTGGAACCTGTGGGAAGACTTCAG 1278
QY 1321 CCTCTGTAGAGAGGCGAGAGATGGTTCATCCAGAGATCCACAGTCCAGTTCAT 1380
DB 1279 CCTCTGTAGAGAGGCGAGAGATGGTTCATCCAGAGATCCACAGTCCAGTTCAT 1338
QY 1381 CATTTGTGTTTGTTCAAAAGGTATGAAGTATCTTTTGTGACAAAGAACTACAAACACAA 1440
DB 1339 CATTTGTGTTTGTTCAAAAGGTATGAAGTATCTTTTGTGACAAAGAACTACAAACACAA 1398
QY 1441 AGGAGTGGCGAGGCTCGGGAAAGGAGAGCTCTTCTGTGGCGGTGTGAGCAATTCG 1500
DB 1399 AGGAGTGGCGAGGCTCGGGAAAGGAGAGCTCTTCTGTGGCGGTGTGAGCAATTCG 1458
QY 1501 CGAAAGCTCCGAGGCGCAAGCAGAGTTCGTCCGCGGCTCAGCAAGTTTATCGCGT 1560
DB 1459 CGAAAGCTCCGAGGCGCAAGCAGAGTTCGTCCGCGGCTCAGCAAGTTTATCGCGT 1518
QY 1561 CTACTTTGATTTATCTCGGAGGAGAGCTCCCGGTATCTTAGACCTGAGTACCAAGTGA 1620
DB 1519 CTACTTTGATTTATCTCGGAGGAGAGCTCCCGGTATCTTAGACCTGAGTACCAAGTGA 1578
QY 1621 CAGACTCATGACAAATTTCTCAGCTGTGTTCCACTGTGCACTCCGAGACCAAGGCT 1680
DB 1579 CAGACTCATGACAAATTTCTCAGCTGTGTTCCACTGTGCACTCCGAGACCAAGGCT 1638
QY 1681 CCAGAGCCGGGCGAGCACACGCGAGCGGAGAGAGGAACTACTTCCGAGCAAGCTC 1740
DB 1639 CCAGAGCCGGGCGAGCACACGCGAGCGGAGAGAGGAACTACTTCCGAGCAAGCTC 1698

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QY 1741 AGCGCGTCCCTATACGTGCGCATTTGCAACATGCACCAGTTTATTACGAGGAGCCCGA 1800
DB |||||||
QY 1699 AGCGCGTCCCTATACGTGCGCATTTGCAACATGCACCAGTTTATTACGAGGAGCCCGA 1758
DB |||||||
QY 1801 CTGTTTGGAAAGCAGTTTCCTTCCCTCCATCCTCTCCATCTGCGCTACCGGAGCCAGT 1860
DB |||||||
QY 1759 CTGTTTGGAAAGCAGTTTCCTTCCCTCCATCCTCTCCATCTGCGCTACCGGAGCCAGT 1818
DB |||||||
QY 1861 CTTGAGAGAAATTTGATTCGGGCTTGTTTAAATGATGTCATGTCGAACACAGGCGCTGA 1920
DB |||||||
QY 1819 CTTGAGAGAAATTTGATTCGGGCTTGTTTAAATGATGTCATGTCGAACACAGGCGCTGA 1878
DB |||||||
QY 1921 GAGTGACTTCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGGCAACCGGACAGCCGACTC 1980
DB |||||||
QY 1879 GAGTGACTTCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGGCAACCGGACAGCCGACTC 1938
DB |||||||
QY 1981 CCAGCAGCAGAGTCAGCATGCGGCGCTTGACCAAGACGGGAGGCGCGCTGCGCTTGA 2040
DB |||||||
QY 1939 CCAGCAGCAGAGTCAGCATGCGGCGCTTGACCAAGACGGGAGGCGCGCTGCGCTTGA 1998
DB |||||||
QY 2041 CGGTAGCGCCGCTGCAACCCCTGCTGCACACCGTGAAACCGGACGCGCTCGGACAT 2100
DB |||||||
QY 1999 CGGTAGCGCCGCTGCAACCCCTGCTGCACACCGTGAAACCGGACGCGCTCGGACAT 2058
DB |||||||
QY 2101 GCCGCGGACTCAGGCATCTATGACTGCTGTCGCTCATCCGAGCTGTCTCTGCCACT 2160
DB |||||||
QY 2059 GCCGCGGACTCAGGCATCTATGACTGCTGTCGCTCATCCGAGCTGTCTCTGCCACT 2118
DB |||||||
QY 2161 GATGAAGGACTCTCGACGACCAAGAACAGTCTTCCCTGACGGAGACGCTGTCCTC 2220
DB |||||||
QY 2119 GATGAAGGACTCTCGACGACCAAGAACAGTCTTCCCTGACGGAGACGCTGTCCTC 2178
DB |||||||
QY 2221 CTCTTCAGGCGCTGGTGAGGAGAACCTCTCTGCGCTTCCCTTCCAGCTCTCTCTCTGG 2280
DB |||||||
QY 2179 CTCTTCAGGCGCTGGTGAGGAGAACCTCTCTGCGCTTCCCTTCCAGCTCTCTCTCTGG 2238
DB |||||||
QY 2281 GTCATGCAAGCAGACTCTTGTGTGCGCAGCTACACTGATGAACCTCCACGGGCTCGCCCC 2340
DB |||||||
QY 2239 GTCATGCAAGCAGACTCTTGTGTGCGCAGCTACACTGATGAACCTCCACGGGCTCGCCCC 2298
DB |||||||
QY 2341 TTTGTAAACAAACGAAAGAGCTTAAGCAATTGCCACTTTAGCTG 2383
DB |||||||
QY 2299 TTTGTAAACAAACGAAAGAGCTTAAGCAATTGCCACTTTAGCTG 2341
DB |||||||
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RESULT 4

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AAS18134
ID AAS18134 standard; cDNA; 2786 BP.
XX
AC AAS18134;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX cytokine receptor subunit 8 (DCRS8) cDNA.
XX
KW Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; ss;
XX gene therapy; protein therapy; immunological disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 70..2286
FT /*tag= a
FT /product= "Human DCRS8"
XX
XX WO200190358-A2.
XX
XX 29-NOV-2001.
XX
XX 23-MAY-2001; 2001WO-US016767.
XX
XX 24-MAY-2000; 2000US-0206862P.
XX
XX
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(SCHE) SCHERING CORP.

Gorman DM;

WPI; 2002-106198/14.

P-PSDB; AAU11355.

Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders.

Claim 16; Page 21-25; 148pp; English.

The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the human DCRS8 polypeptide

SQ Sequence 2786 BP; 673 A; 760 C; 709 G; 637 T; 0 U; 7 Other;

Query Match 93.1%; Score 2218.6; DB 6; Length 2786;

Best Local Similarity 97.2%; Pred. No. 0;

Matches 2292; Conservative 0; Mismatches 20; Indels 45; Gaps 2;

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QY 27 CTGCCCAGCGCGCGCGCGCGCGCGCGCGCAGAGACGGCTGGCTGGCGAGCGCAGCGCA 86
DB |||||||
DB 11 CGGCGCCAGCAGCGCGCGCGCGCGCGCGCGCAGAGACGGCTGGCTGGCGAGCGCAGCGCA 70
QY 87 TGGCCCCGCTGGCTGACGCTCTGCTCGCTCTTCTTACGGTCAACGCTGCTCAACGGCT 146
DB |||||||
DB 71 TGGCCCCGCTGGCTGACGCTCTGCTCGCTCTTCTTACGGTCAACGCTGCTCAACGGCT 130
QY 147 CGCAGCTGGCTGTGGCGCGCTGGCGGGTCCGCGCCGCGCGCGCGCGCAGACCTGTGGCT 206
DB |||||||
DB 131 CGCAGCTGGCTGTGGCGCGCTGGCGGGTCCGCGCCGCGCGCGCGCAGACCTGTAGCT 190
QY 207 GGAGGATGAAGCGGCTGCGCGACCCCGGCTTGTGTGTTAATGAGGGAGTGGGGCCAG 266
DB |||||
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DB 191 GGA-----NCGGAGTGGGGCCAG 208
QY 267 CCAGCAGAAACAGTGGGCTGTACAAACATCACCTTCAAATATGACAAATGTACCACTACT 326
DB |||||||
DB 209 CCAGCAGAAACAGTGGGCTGTACAAACATCACCTTCAAATATGACAAATGTACCACTACT 268
QY 327 TGAATCCAGTGGGGAAGCATGTGATTCTGACGCCAGAAATATCACCATCAGCAGATATG 386
DB |||||||
DB 269 TGAATCCAGTGGGGAAGCATGTGATTCTGACGCCAGAAATATCACCATCAGCAGATATG 328
QY 387 CTTGCCATGACCAAGTGGCAGTCAACATTTCTTGGTCCCGAGGGGCGCTCGGCATCGAAT 446
DB |||||||
DB 329 CTTGCCATGACCAAGTGGCAGTCAACATTTCTTGGTCCCGAGGGGCGCTCGGCATCGAAT 388
QY 447 TCCTGAAAGGATTTTCGGGTAACTACTGGAGGAGCTGAAAGTCCGAGGGAAGACAGATGCCAAC 506
DB |||||||
DB 389 TCCTGAAAGGATTTTCGGGTAACTACTGGAGGAGCTGAAAGTCCGAGGGAAGACAGATGCCAAC 448
QY 507 AACTGATTTCTAAAGGATCCGAAAGCAGCTCAACAGTAGCTTCAAAGAACTCGGAATGGAAT 566
DB |||||||
DB 449 AACTGATTTCTAAAGGATCCGAAAGCAGCTCAACAGTAGCTTCAAAGAACTCGGAATGGAAT 508
QY 567 CTCAACCTTTCTGAAATATGAAATTTGAAACGGGATTTTGGTAAAGGTTCTCCCTTTTC 626
DB |||||||
DB 509 CTCAACCTTTCTGAAATATGAAATTTGAAACGGGATTTTTCGTAAGG---TTGCTCTTTT 565
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QY 627 CTTTCATTAATAAAGCAATTAACACCCCTTTCTTTTAGAACCCGAGCTGTGACC 686
DB 566 CTTTCATTAATAAAGCAATTAACACCCCTTTCTTTTAGAACCCGAGCTGTGACC 625
QY 687 TGTGTTTACAGCCGAGCAATCTAGCTTGTAAACCTTCTTGAAGCCTCGGAACCTGAACA 746
DB 626 TGTGTTTACAGCCGAGCAATCTAGCTTGTAAACCTTCTTGAAGCCTCGGAACCTGAACA 685
QY 747 TCAGCCAGCATGGCTCGGACATGCAAGTGTCTTCGACCATGCAACCCGACAACTTCGGCT 806
DB 686 TCAGCCAGCATGGCTCGGACATGCAAGTGTCTTCGACCATGCAACCCGACAACTTCGGCT 745
QY 807 TCCGTTTCTTCTATCTTCACTAAGAGCTCAAGCAGGAAGACCTTTCAAGCGAAGACCT 866
DB 746 TCCGTTTCTTCTATCTTCACTAAGAGCTCAAGCAGGAAGACCTTTCAAGCGAAGACCT 805
QY 867 GTAAGCAGAGCAAACTACAGAGACGACGAGTGTCTTCAAAATGTTTTCAGGGG 926
DB 806 GTAAGCAGAGCAAACTACAGAGATGACGAGTGTCTTCAAAATGTTTTCAGGGG 865
QY 927 ATTATATAATTGAGTGTGGATGACCTTAACACAAAGAAAGTGTGATGATGCT 986
DB 866 ATTATATAATTGAGTGTGGATGACCTTAACACAAAGAAAGTGTGATGATGCT 925
QY 987 TAAAGCCAGTGCACCTCCCGTGGCGGCCCATCAGAGCCGTGCGCATCACAGTGCCAC 1046
DB 926 TAAAGCCAGTGCACCTCCCGTGGCGGCCCATCAGAGCCGTGCGCATCACAGTGCCAC 985
QY 1047 TGGTAGTCATATCGGCATTCGCGACGCTTTCACCTGTGATGTGCGCGCAAGCAACAAG 1106
DB 986 TGGTAGTCATATCGGCATTCGCGACGCTTTCACCTGTGATGTGCGCGCAAGCAACAAG 1045
QY 1107 AAAATATATATTCATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGACGAC 1166
DB 1046 AAAATATATATTCATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGACGAC 1105
QY 1167 TCCCAAGAGAGAGGCTCCGCGCGCGCGCAAGGTCTTCTGCTATTCCAGTAAAGATG 1226
DB 1106 TCCCAAGAGAGAGGCTCCGCGCGCGCGCAAGGTCTTCTGCTATTCCAGTAAAGATG 1165
QY 1227 GCCAGAAATCATAATGATGCTGCTCAAGTGTTCGCTTCTTCCAGGACTTCTGTGCT 1286
DB 1166 GCCAGAAATCATAATGATGCTGCTCAAGTGTTCGCTTCTTCCAGGACTTCTGTGCT 1225
QY 1287 GTGAGGTGCTCTGACCTGTGGAGAGACTTCAGGCTCTGTAGAGAGGGCAGAGAAAT 1346
DB 1226 GTGAGGTGCTCTGACCTGTGGAGAGACTTCAGGCTCTGTAGAGAGGGCAGAGAAAT 1285
QY 1347 GGGTCATCCAGAGATCCACGAGTCCAGTTCATTCATGTTGTTTCCAAAGGTATGA 1406
DB 1286 GGGTCATCCAGAGATCCACGAGTCCAGTTCATTCATGTTGTTTCCAAAGGTATGA 1345
QY 1407 AGTACTTTGTGACAAAGAACTACAAACAAAGAGGAGTGGCCGAGGCTCGGGGAAAG 1466
DB 1346 AGTACTTTGTGACAAAGAACTACAAACAAAGAGGAGTGGCCGAGGCTCGGGGAAAG 1405
QY 1467 GAGAGCTCTTCTGTGGGGGTGTAGCCATTCGCGAAAGCTCCGCGAGGCAAGCAGA 1526
DB 1406 GAGAGCTCTTCTGTGGGGGTGTAGCCATTCGCGAAAGCTCCGCGAGGCAAGCAGA 1465
QY 1527 GTTCGTCGCGGGGCTCAGCAAGTTTATCGCGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1586
DB 1466 GTTCGTCGCGGGGCTCAGCAAGTTTATCGCGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1525
QY 1587 AGCTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGGAACATCTTCTCTCAGC 1646
DB 1526 AGCTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGGAACATCTTCTCTCAGC 1585
QY 1647 TCTGTTTCCACTTGCACTCCCGAGACCAAGGCTCCAGAGCCGGGCGAGCAAGCGGAC 1706
DB 1586 TCTGTTTCCACTTGCACTCCCGAGACCAAGGCTCCAGAGCCGGGCGAGCAAGCGGAC 1645
QY 1707 AGGGCAGCAGAGGAAGTACTTCCGGAGCAAGTTCAGGCGGTCCCTATAGCTCGCAATTT 1766
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DB 1646 AGGGCAGCAGAGGAAGTACTTCCGGAGCAAGTTCAGGCGGTCCCTATACGTCGCAATTT 1705
QY 1767 GCAACATGCACAGTTTATTCACGAGGAGCCGACTGTTTCGAAAGCAGTTCGTTCCCT 1826
DB 1706 GCAACATGCACAGTTTATTCACGAGGAGCCGACTGTTTCGAAAGCAGTTCGTTCCCT 1765
QY 1827 TCCATCTCTCTCCACTGCGCTACCGGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTGG 1886
DB 1766 TCCATCTCTCTCCACTGCGCTACCGGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTGG 1825
QY 1887 TTTTAAATGATGTCATGTGCAAAACGAGGCTGAGAGTACTTCTGCTTAAAGGTAGAGG 1946
DB 1826 TTTTAAATGATGTCATGTGCAAAACGAGGCTGAGAGTACTTCTGCTTAAAGGTAGAGG 1885
QY 1947 CGGCTGTTCTTGGGGCAACCGGACCGAGCTCCACGACGAGAGTCCAGATGGGGCC 2006
DB 1886 CGGCTGTTCTTGGGGCAACCGGACCGAGCTCCACGACGAGAGTCCAGATGGGGCC 1945
QY 2007 TGGACCAAGACGGGGAGCCCGGCTGCTTTCGAGTGGCGCCCTTGCAACCCCTGC 2066
DB 1946 TGGACCAAGACGGGGAGCCCGGCTGCTTTCGAGTGGCGCCCTTGCAACCCCTGC 2005
QY 2067 TGCACACGGTGAAAGCCGCGAGCCCTCGGACATGCGCGGGACTCAGGCACTTATGACT 2126
DB 2006 TGCACACGGTGAAAGCCGCGAGCCCTCGGACATGCGCGGGACTCAGGCACTTATGACT 2065
QY 2127 CGTCTGTGCTTCATCCGAGTGTCTGCGACATGATGGAAGGACTCTCGAGGACCGAGA 2186
DB 2066 CGTCTGTGCTTCATCCGAGTGTCTGCGACATGATGGAAGGACTCTCGAGGACCGAGA 2125
QY 2187 CAGAAACCTCTTCCCTGACGAGAGCGTGTCTCTCTTCAGGCTGGGTGAGGAGAAC 2246
DB 2126 CAGAAACCTCTTCCCTGACGAGAGCGTGTCTCTCTTCAGGCTGGGTGAGGAGAAC 2185
QY 2247 CTCTGCGCTTCTTCCAAAGTCTCTCTTCTGCGTATGCAAGACAGATCTTGGTTGCC 2306
DB 2186 CTCTGCGCTTCTTCCAAAGTCTCTCTTCTGCGTATGCAAGACAGATCTTGGTTGCC 2245
QY 2307 GCAGTACACTGATGAACTCCACGCGGTGCGCCCTTGTACAAACCGAAAGAGTCTAAG 2366
DB 2246 GCAGTACACTGATGAACTCCACGCGGTGCGCCCTTGTACAAACCGAAAGAGTCTAAG 2305
QY 2367 CATTGCCACTTTAGCTG 2383
DB 2306 CATTGCCACTTTAGCTG 2322
RESULT 5
AAS15346
ID AAS15346 standard; cDNA; 3083 BP.
XX
AC AAS15346;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding human Interleukin 17 (hIL-17) receptor like protein.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 22..2235
FT /*tag= a
FT /product= "Interleukin 17 (IL-17) receptor like protein"
FT /partial
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FT XX /note= "No stop codon given"
PN XX
XX W0200168859-A2.
PD XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-US008678.
XX
XX 16-MAR-2000; 2000US-0189816P.
PR XX 28-NOV-2000; 2000US-00724460.
XX
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
PI XX
XX WPI; 2001-611392/70.
DR P-PSDB; AAU09904.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT psoriasis and glaucoma.
XX
XX Claim 1; Page 147-148,150-151; 158pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
CC ophthalmological activities. The IL-17 receptor like nucleic acids and
CC proteins may be used to prevent and treat diseases associated with
CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicemia),
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis), cancers (e.g. leukaemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quanticate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity. This sequence encodes the human Interleukin 17
CC (IL-17) receptor like protein described in the method of the invention
XX
SQ Sequence 3083 BP; 782 A; 807 C; 767 G; 727 T; 0 U; 0 Other;

Query Match 93.0%; Score 2215.4; DB 4; Length 3083;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2271; Conservative 0; Mismatches 6; Indels 42; Gaps 1;

Qy 65 TGGCTGGGCGAGCGCAGCGCCATGGCCCGCTGGCTGCAGCTCTGCTCCGCTTCTTTACG 124
Db 1 TGGCTGGGCGAGCGCAGCGCCATGGCCCGCTGGCTGCAGCTCTGCTCCGCTTCTTTACG 60

Qy 125 GTCACGCGCTGCTCAACGGCTCGCAGCTGGCTGTGGCGCGCTGGCGGGTCCGGCGCGCG 184
Db 61 GTCACGCGCTGCTCAACGGCTCGCAGCTGGCTGTGGCGCGCTGGCGGGTCCGGCGCGCG 120

Qy 185 CGGCGCGCGACACCTGTGGCTGGAGGATGAAGCGGCTGCCGACCCCGCTTTGTGTT 244
Db 121 TGGGCGGTGCAACCTGTGGCTGGAG-----146

Qy 245 GCTAATGAGGGAGTGGGCGCGACCCAGCAGAAACAGTGGGCTGTACAAATCACCTTCAA 304
Db 147 -----GGGAGTGGGCGCGACCCAGCAGAAACAGTGGGCTGTACAAATCACCTTCAA 198

305 TATGACAAATTGTACCACTCTTGAATCCAGTGGGGAAGCATGTGATTGCTGAAGCCGAC 364
199 TATGACAAATTGTACCACTCTTGAATCCAGTGGGGAAGCATGTGATTGCTGAAGCCGAC 258
365 AATATCACCATCAGCCAGTATGCTTGCATGACCAAGTGGCAGTCACCAATCTTTTGGTCC 424
259 AATATCACCATCAGCCAGTATGCTTGCATGACCAAGTGGCAGTCACCAATCTTTTGGTCC 318
425 CCAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTAATTAATCTGGAGGAGCTGAAG 484
319 CCAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTAATTAATCTGGAGGAGCTGAAG 378
485 TCGGAGGGAAGACAGTGCACCAACTGATTTCTAAAGGATCCGAAGCAGCTCAAACAGTAGC 544
379 TCGGAGGGAAGACAGTGCACCAACTGATTTCTAAAGGATCCGAAGCAGCTCAAACAGTAGC 438
545 TTCAAAAGAACTGGAATGGAATCTCAACCTTTCTGAAATGAAATTTGAAACGGATTAT 604
439 TTCAAAAGAACTGGAATGGAATCTCAACCTTTCTGAAATGAAATTTGAAACGGATTAT 498
605 TTCTGAAAGGTTGTCCTTTTCTTCCATTAAAAACGAAAGCAATTTACCACCTTTCTTTC 664
499 TTCTGAAAGGTTGTCCTTTTCTTCCATTAAAAACGAAAGCAATTTACCACCTTTCTTTC 558
665 TTTAGAACCCGAGCCTGTGACCTGTGTTACAGCCGGACCAATCTAGCTTTGTAACCCCTTC 724
559 TTTAGAACCCGAGCCTGTGACCTGTGTTACAGCCGGACCAATCTAGCTTTGTAACCCCTTC 618
725 TGGAAAGCCTCGGAACCTGGAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTCGAC 784
619 TGGAAAGCCTCGGAACCTGGAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTCGAC 678
785 CATGCAACCGCAAACTCTGGCTTCGGCTTCTTCTATCTTCACTCAAGCTCAAGCAGAA 844
679 CACGACCGCAAACTCTGGCTTCGGCTTCTTCTATCTTCACTCAAGCTCAAGCAGAA 738
845 GGACCTTTCAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACGAGCTGCCTC 904
739 GGACCTTTCAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACGAGCTGCCTC 798
905 CTTCAAAATGTTTCTCCAGGGGATTATATAATTTAGCTGGTGGATGACACTAAACACA 964
799 CTTCAAAATGTTTCTCCAGGGGATTATATAATTTAGCTGGTGGATGACACTAAACACA 858
965 AGAAAGTATGATATGATGCTTTAAAGCAGTGCATCTCCCGTGGCGGCGGCCATCAGA 1024
859 AGAAAGTATGATGATGCTTTAAAGCAGTGCATCTCCCGTGGCGGCGGCCATCAGA 918
1025 GCCGTGGCCATCAGTGGCCATCGGTAGTATATCGGCATTCGCGAGCTCTTCACTGTG 1084
919 GCCATGGCCATCAGTGGCCATCGGTAGTATATCGGCATTCGCGAGCTCTTCACTGTG 978
1085 ATGTGCGCGAAGAGCAACAGAAATATATATTTACATTTAGATGAAGAGAGCTCTGAG 1144
979 ATGTGCGCGAAGAGCAACAGAAATATATATTTACATTTAGATGAAGAGAGCTCTGAG 1038
1145 TCTTCCACATACACTGACGACCTCCCAAGAGAGAGGCTCCGCGCGCGCGGAGAGTCTTT 1204
1039 TCTTCCACATACACTGACGACCTCCCAAGAGAGAGGCTCCGCGCGCGCGGAGAGTCTTT 1098
1205 CTCTGCTATTCCAGTAAAGATGGCCAGNACACATGAATGCTGCTCCAGTGTTCGCTTAC 1264
1099 CTCTGCTATTCCAGTAAAGATGGCCAGNACACATGAATGCTGCTCCAGTGTTCGCTTAC 1158
1265 TTCTCCAGGACTTCTGTGGCTGTGAGTGGCTCTGGACCTGTGGGAGAGCTTCAGGCTC 1324
1159 TTCTCCAGGACTTCTGTGGCTGTGAGTGGCTCTGGACCTGTGGGAGAGCTTCAGGCTC 1218
1325 TGTAGAGAGGGCAGAGAGAAATGGGTATCCAGAAAGATCCACGAGTCCAGTTCATCAT 1384
1219 TGTAGAGAGGGCAGAGAGAAATGGGTATCCAGAAAGATCCACGAGTCCAGTTCATCAT 1278

Qy	2302	TTGCCGAGCTACACTGATGAACTCCACGGGTCGCCCTTGTGTAA	CAAAACGAAAGAGT	2361
Db	2179	TTGCCGAGCTACACTGATGAACTCCACGGGTCGCCCTTGTGTAA	CAAAACGAAAGAGT	2238
Qy	2362	CTAAGCATTTGCCACTTTAGCTG	2383	
Db	2239	CTAAGCATTTGCCACTTTAGCTG	2260	

RESULT 7	
ADB63275	
ID	ADB63275 standard; cDNA; 2894 BP.
XX	
XX	
AC	ADB63275;
XX	
XX	04-DEC-2003 (first entry)
DT	
XX	
XX	Human cDNA encoding clone TESTI20046540.
DE	
XX	
XX	Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
KW	tissue regeneration; cell regeneration; membrane protein;
KW	signal transduction-related protein; transcription-related protein;
KW	osteoporosis; neurological disease; cancer; tumour.
XX	
OS	Homo sapiens.

PH	Key	Location/Qualifiers
FT	CDS	123..2309
FT		/*tag= a
FT		/product= "Clone TESTI20046540 protein"
XX		
XX	EP1308459-A2.	
XX		
XX	07-MAY-2003.	
PD		
XX		
XX	28-MAR-2002; 2002EP-00007401.	
XX		
XX	05-NOV-2001; 2001JP-00379298.	
PR	25-JAN-2002; 2002US-00350378.	
XX		
XX	(HELI-) HELIX RES INST.	
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	
XX		
PI	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;	
PI	Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;	
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;	
XX		
XX	WPI; 2003-450961/43.	
DR	P-PSDB; ADB65245.	
DR		
XX		
PT	New polynucleotides and polypeptides, useful for developing a diagnostic	
PT	marker or medicines for regulation of their expression and activity, or	
PT	as targets of gene therapy.	
XX		
PS	Claim 1; Page: 222pp; English.	

The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes

CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a cDNA of the invention. Note: Some of the sequence
CC data for this patent is not represented in the printed specification, but
CC is based on sequence information supplied by the European Patent Office.
XX
Sequence 2894 BP: 735 A; 751 C; 730 G; 678 T; 0 U; 0 Other

Query Match	89.3%	Score 2128	DB 10	Length 2894
Best Local Similarity	98.6%	Pred. No. 0		
Matches 2146	Conservative	0	Mismatches 30	Indels 0
QY	208	GAGGATCAAAAGCGGTGCCCGACCCCGGCTTTGTGTGCTTAATGAGGGAGTGGGGCCAGC	267	
DB	170	GTGGCTGAAGAGTGTGGCTGGAATTACAGGCAATCCTGGCCTTGGCAGGGAGTGGGCCAGC	229	
QY	268	CAGCAGAAAACAGTGGGCTGTACAACATCACCTTTCAAATATGACAAATGTGTACCACTTACTT	327	
DB	230	CAGCAGAAAACAGTGGGCTGTACAACATCACCTTTCAAATATGACAAATGTGTACCACTTACTT	289	
QY	328	GAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAAATATCACCATCAGCCAGTATGC	387	
DB	290	GAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAAATATCACCATCAGCCAGTATGC	349	
QY	388	TTGCGCATGACCAAGTGCAGTCAACCATTTCTTGGTCCCGAGGGGCCCTCGGCATCGAATT	447	
DB	350	TTGCGCATGACCAAGTGCAGTCAACCATTTCTTGGTCCCGAGGGGCCCTCGGCATCGAATT	409	
QY	448	CCTGAAAAGGATTTCCGGTAAATCTCTGGAGGAGCTGAAATCGGAGGGGAAGACAGTGCACAACA	507	
DB	410	CCTGAAAAGGATTTCCGGTAAATCTCTGGAGGAGCTGAAATCGGAGGGGAAGACAGTGCACAACA	469	
QY	508	ACTGATTTCTAAAGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGACCTGGAATGGAAATC	567	
DB	470	ACTGATTTCTAAAGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGACCTGGAATGGAAATC	529	
QY	568	TCAACCTTTCTCTGAATATGAAATTTGAAACCGGATTTATTCGTAAAGGTTGTCCCTTTTCC	627	
DB	530	TCAACCTTTCTCTGAATATGAAATTTGAAACCGGATTTATTCGTAAAGGTTGTCCCTTTTCC	589	
QY	628	TTCCATTTAAAAACGAAAGCAATTACCAACCTTTCTCTTTTAGAACCCGAGCCTGTGACCT	687	
DB	590	TTCCATTTAAAAACGAAAGCAATTACCAACCTTTCTCTTTTAGAACCCGAGCCTGTGACCT	649	
QY	688	GTGTGTTACAGCCGGAACAATCTAGCTTTGTAACCCCTTCTGGAAGCCTCGGAACCTGACAT	747	
DB	650	GTGTGTTACAGCCGGAACAATCTAGCTTTGTAACCCCTTCTGGAAGCCTCGGAACCTGACAT	709	
QY	748	CAGCCAGCATGGCTCGGACATGACAGGTGTCTCTTCGACCATGCACCGCACAACTTCGGCTT	807	
DB	710	CAGCCAGCATGGCTCGGACATGACAGGTGTCTCTTCGACCATGCACCGCACAACTTCGGCTT	769	
QY	808	CCGTTTCTTCTATCTTCACTACAAGCTCAAGCAGAGGACCTTTCAAGCGAAAGACCTG	867	
DB	770	CCGTTTCTTCTATCTTCACTACAAGCTCAAGCAGAGGACCTTTCAAGCGAAAGACCTG	829	
QY	868	TAAGCAGGAGCAAACTACAGAGCAGACCGACCTGCTCTTCAAAATGTTTCTCCAGGGGA	927	
DB	830	TAAGCAGGAGCAAACTACAGAGATGACCGCTGCTCTTCAAAATGTTTCTCCAGGGGA	889	
QY	928	TTATATAATTTGAGCTGGTGGATGACACTAAACAAAGAAAAGTGTATGATTTATGCTT	987	
DB	890	TTATATAATTTGAGCTGGTGGATGACACTAAACAAAGAAAAGTGTATGATTTATGCTT	949	
QY	988	AAAGCCAGTGCATCTCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATCAACAGTGCACCT	1047	
DB	950	AAAGCCAGTGCATCTCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATCAACAGTGCACCT	1009	
QY	1048	GGTAGTCAATATCGGCATTCGGGAGCTTCTTCACTGTGATGTCGCCGAAGGACCAAGA	1107	
DB	1010	GGTAGTCAATATCGGCATTCGGGAGCTTCTTCACTGTGATGTCGCCGAAGGACCAAGA	1069	

Db 98 ATTTGACCACTTACTGTAATCCAGTGGGGAAGCATGTGATTTGCTGAGCCGCCAGAAATATCA 157
Qy 372 CCATCAGCAGTATGCTCTTGGCATGACCAAGTGGCAGTACCAATCTTTTGGTCCCGAGGG 431
Db 158 CCATCAGCAGTATGCTCTTGGCATGACCAAGTGGCAGTACCAATCTTTTGGTCCCGAGGG 217
Qy 432 CCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGGAGAGCTGAAGTCGGAGG 491
Db 218 CCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGGAGAGCTGAAGTCGGAGG 277
Qy 492 GAAGCAGTGCACAACTGATTTTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 551
Db 278 GAAGCAGTGCACAACTGATTTTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 337
Qy 552 GAACTGGAATGGAATCTCAACCTTCTTGAATATGAAATTTGAAACCGATTAATTCGTAA 611
Db 338 GAACTGGAATGGAATCTCAACCTTCTTGAATATGAAATTTGAAACCGATTAATTCGTAA 397
Qy 612 AGGTTGTCCTTTCTTCCATTAATAAAGCAATTAACACCTTTCTTTTAGAA 671
Db 398 AGGTTGTCCTTTCTTCCATTAATAAAGCAATTAACACCTTTCTTTTAGAA 457
Qy 672 CCGAGCCTGTGACCTGTTGTTACAGCCGACAAATCTAGCTTGTAAACCTTCTGGAAGC 731
Db 458 CCGAGCCTGTGACCTGTTGTTACAGCCGACAAATCTAGCTTGTAAACCTTCTGGAAGC 517
Qy 732 CTGGAACCTGAACTAGCAGCAGTGGTGGACATGAGTGTCTTTCAGCAATGAC 791
Db 518 CTGGAACCTGAACTAGCAGCAGTGGTGGACATGAGTGTCTTTCAGCAATGAC 577
Qy 792 CGCAAACTTCGGCTTCGGTTCTTCTATCTTCACTACAAGCTCAAGCAGCAAGGACCTT 851
Db 578 CGCAAACTTCGGCTTCGGTTCTTCTATCTTCACTACAAGCTCAAGCAGCAAGGACCTT 637
Qy 852 TCAAGCGAAAGACTGTGAGAGAGGAACTACAGAGAGCAGCTGCTCTCTTCAAA 911
Db 638 TCAAGCGAAAGACTGTGAGAGAGGAACTACAGAGATGACCACTGCTCTCTTCAAA 697
Qy 912 ATGTTTCTCCAGGGATTAATAATGAGCTGGTGAGTGAACACTAACACAAAGAAAG 971
Db 698 ATGTTTCTCCAGGGATTAATAATGAGCTGGTGAGTGAACACTAACACAAAGAAAG 757
Qy 972 TGATGATTAATGCTTAAAGCCAGTGCATCTCCCGTGGCGCCGACATCAGAGCCGTGG 1031
Db 758 TGATGATTAATGCTTAAAGCCAGTGCATCTCCCGTGGCGCCGACATCAGAGCCGTGG 817
Qy 1032 CCATCAGTGCACCTGCTAGTGCATATCGGCATTCGCGAGCTCTTCACTGTGATGTGCC 1091
Db 818 CCATCAGTGCACCTGCTAGTGCATATCGGCATTCGCGAGCTCTTCACTGTGATGTGCC 877
Qy 1092 GCAAGAGCAACAGAAATATATATTCATTTAGATGAAGAGCTCTGAGTCTTCCA 1151
Db 878 GCAAGAGCAACAGAAATATATATTCATTTAGATGAAGAGCTCTGAGTCTTCCA 937
Qy 1152 CATACACTGACACTCCCAAGAGAGAGCTCCGCGCGCGGAGGCTTTCTCTGCT 1211
Db 938 CATACACTGACACTCCCAAGAGAGAGCTCCGCGCGCGGAGGCTTTCTCTGCT 997
Qy 1212 ATTCAGTAAGATGCCAGAAATCAATGAATGTGTCAGTGTTCGCTACTTCTCTCC 1271
Db 998 ATTCAGTAAGATGCCAGAAATCAATGAATGTGTCAGTGTTCGCTACTTCTCTCC 1057
Qy 1272 AGGACTTCTGTGGTGTGAGGTGGCTTGGACCTGTGGGAAGACTTCAGCCTCTGAG 1331
Db 1058 AGGACTTCTGTGGTGTGAGGTGGCTTGGACCTGTGGGAAGACTTCAGCCTCTGAG 1117
Qy 1332 AAGGCGAGAGAAATGGGTTCATCCAGAGATCCAGTCCAGTTCATCATTTGGTTT 1391
Db 1118 AAGGCGAGAGAAATGGGTTCATCCAGAGATCCAGTCCAGTTCATCATTTGGTTT 1177
Qy 1392 GTTCCAAAGGTATGAAGTACTTTGTGGCAAGAAGAACTTACAAACACAAAGGAGGTGCC 1451

Db 1178 GTTCCAAAGGTATGAAGTACTTTTGGACAGAAGAACTACAAACACAAAGGAGGTGCC 1237
Qy 1452 GAGGCTCGGGAAAGGAGAGCTCTTCTGTGGGGGTTCAGCCATTGCCGAAAAGCTCC 1511
Db 1238 GAGGCTCGGGAAAGGAGAGCTCTTCTGTGGGGGTTCAGCCATTGCCGAAAAGCTCC 1297
Qy 1512 GCGAGGCCAAGCAGAGTTCTGTCGGGGGCTCAGCAAGTTTATCGCCGCTACTTTGATT 1571
Db 1298 GCGAGGCCAAGCAGAGTTCTGTCGGGGGCTCAGCAAGTTTATCGCCGCTACTTTGATT 1357
Qy 1572 ATTCTCGAGGGAGAGCTCCCGGTATCTCTAGACTGAGTACCAAGTACAGACTCATGG 1631
Db 1358 ATTCTCGAGGGAGAGCTCCCGGTATCTCTAGACTGAGTACCAAGTACAGACTCATGG 1417
Qy 1632 ACAATCTTCTCAGCTCTGTTTCCCACTTCCGAGACCAAGCTTCAGAGAGCCGG 1691
Db 1418 ACAATCTTCTCAGCTCTGTTTCCCACTTCCGAGACCAAGCTTCAGAGAGCCGG 1477
Qy 1692 GCGAGCACCGGACAGGGGAGCAGAAAGTACTTCCGGAGCAAGTCAAGCCGGTCCC 1751
Db 1478 GCGAGCACCGGACAGGGGAGCAGAAAGTACTTCCGGAGCAAGTCAAGCCGGTCCC 1537
Qy 1752 TATAGCTCGCATTTGCAACATGCAACAGTTTATTGACGAGAGCCCGACTGGTTTCAAAA 1811
Db 1538 TATAGCTCGCATTTGCAACATGCAACAGTTTATTGACGAGAGCCCGACTGGTTTCAAAA 1597
Qy 1812 AGCAGTTCTGTTTCCCTTCCATCTCTCCACTGCGTACCGGAGCCAGCTTTGGAGAAAT 1871
Db 1598 AGCAGTTCTGTTTCCCTTCCATCTCTCCACTGCGTACCGGAGCCAGCTTTGGAGAAAT 1657
Qy 1872 TTGATTCCGGCTTGGTTTAAATGATGTGCAAAACCGAGGCTGAGAGTGAATCT 1931
Db 1658 TTGATTCCGGCTTGGTTTAAATGATGTGCAAAACCGAGGCTGAGAGTGAATCT 1717
Qy 1932 GCCTAAAGTATAGCGGCTGTTTCTTGGGGCAACCGGACCGAGCTCCAGCAGCAGAG 1991
Db 1718 GCCTAAAGTATAGCGGCTGTTTCTTGGGGCAACCGGACCGAGCTCCAGCAGCAGAG 1777
Qy 1992 GTCAGACTGGGGGCTCGGACCAAGACGGGGAGCCCGCTGCTTGAAGTACGCGC 2051
Db 1778 GTCAGACTGGGGGCTCGGACCAAGACGGGGAGCCCGCTGCTTGAAGTACGCGC 1837
Qy 2052 CCTTGCAACCCCTGCTGCAACGGTGAAGCCGGAGCCCTCGGACATGCCCGCGGACT 2111
Db 1838 CCTTGCAACCCCTGCTGCAACGGTGAAGCCGGAGCCCTCGGACATGCCCGCGGACT 1897
Qy 2112 CAGGCATCTATGACTCTGCTGCTCCATCCGAGCTGTCTCTGCTGCTGATGGAAGGAC 2171
Db 1898 CAGGCATCTATGACTCTGCTGCTCCATCCGAGCTGTCTCTGCTGCTGATGGAAGGAC 1957
Qy 2172 TCTCGACGGACCAAGACAGAAACGTCTTCCCTGACGGAGAGCGTCTCTCTTCAAGGCC 2231
Db 1958 TCTCGACGGACCAAGACAGAAACGTCTTCCCTGACGGAGAGCGTCTCTCTTCAAGGCC 2017
Qy 2232 TGGGTGAGAGGAACTCTCTGCGCTTCTTCCAAAGCTCTCTCTTCTGCGGTATGCAAG 2291
Db 2018 TGGGTGAGAGGAACTCTCTGCGCTTCTTCCAAAGCTCTCTCTTCTGCGGTATGCAAG 2077
Qy 2292 CAGATCTTGGTTCGCGAGCTACACTGATGAATCCAGCGGTGCGCCCTTTGTAAACAA 2351
Db 2078 CAGATCTTGGTTCGCGAGCTACACTGATGAATCCAGCGGTGCGCCCTTTGTAAACAA 2137
Qy 2352 ACGAAAGAGTCTAAGCATTTGCCATTTAGCTG 2383
Db 2138 ACGAAAGAGTCTAAGCATTTGCCATTTAGCTG 2169

RESULT 9

AAS09517

ID AAS09517 standard; cdna; 2319 BP.

XX

AAS09517;

XX

DT	24-OCT-2001	(first entry)	Query Match	87.0%;	Score 2074.2;	DB 4;	Length 2319;
XX	Human cDNA encoding Interleukin 17 receptor, IL-17RH4.		Best Local Similarity	98.1%;	Pred. No. 0;		
DE			Matches 2125;	Conservative	0;	Mismatches	3;
XX						Indels	39;
XX						Gaps	1;
KW	Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; ss;		252	AGGAGTGGGCGCAGCAGAGAAACAGTGGGTGTACAAATCACCCTTCAATATGACA	311		
KW	PRO20026; DNA 154095-2998; systemic lupus erythematosus;		122	AGGAGTGGGCGCAGCAGAGAAACAGTGGGTGTACAAATCACCCTTCAATATGACA	181		
KW	rheumatoid arthritis; osteoarthritis; diabetes mellitus;		312	ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGAGCCCGAGAAATCA	371		
KW	allergic disease; asthma; demyelinating disease;		182	ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGAGCCCGAGAAATCA	241		
XX	degenerative cartilaginous disorder; transplantation associated disease.						
OS	Homo sapiens.						
XX		Key	372	CCATCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCAACATCTTTTGGTCCCGAGGG	431		
XX		Location/Qualifiers					
PH		CDS					
FT		70..2255					
FT		/*tag= a					
FT		/product= "IL-17RH4"					
XX							
XX	WO200146420-A2.						
XX							
XX	28-JUN-2001.						
XX							
XX	20-DEC-2000; 200WO-US034956.						
PF							
XX							
XX	23-DEC-1999; 99US-0172096P.						
PR	30-DEC-1999; 99WO-US031274.						
PR	11-JAN-2000; 2000US-0175481P.						
PR	18-FEB-2000; 2000WO-US004341.						
PR	02-MAR-2000; 2000WO-US005841.						
PR	21-MAR-2000; 2000WO-US007532.						
PR	02-JUN-2000; 2000WO-US015264.						
PR	22-JUN-2000; 2000US-0213807P.						
PR	22-AUG-2000; 2000US-00644848.						
PR	24-AUG-2000; 2000WO-US023328.						
PR	24-OCT-2000; 2000US-0242837P.						
PR	10-NOV-2000; 2000WO-US030873.						
PR	28-NOV-2000; 2000US-0253646P.						
PR	01-DEC-2000; 2000WO-US032678.						
XX							
XX	(GETH) GENENTECH INC.						
PA							
XX	Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;						
XX	Gurney AL, Li H, Hillan KJ, Tamas D, Van Lookeren M, Vandlen RL;						
PI	Watanabe CK, Williams PM, Wood WI, Yansura DG;						
XX							
XX	WPI; 2001-451708/48.						
DR	P-PSDB; AAU04958.						
XX							
XX	Novel PRO polypeptides homologous to interleukin-17, useful for the						
PT	diagnosis and treatment of immune related disease e.g. rheumatoid						
PT	arthritis and diabetes.						
XX							
XX	Claim 1; Fig 17; 188pp; English.						
PS							
XX							
CC	The sequence (DNA 154095-2998) encodes a PRO polypeptide (PRO20026) which						
CC	is the human Interleukin 17 receptor, IL-17RH4. A composition containing						
CC	ant/agonists to the PRO polypeptides or individual components are useful						
CC	for treating a mammal with an immune related disease, e.g. systemic lupus						
CC	erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic						
CC	arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic						
CC	inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,						
CC	sarcoidosis, autoimmune hemolytic anaemia, autoimmune thrombocytopaenia,						
CC	thyroiditis, diabetes mellitus, immune-mediated renal disease, a						
CC	demyelinating disease, an autoimmune or immune-mediated skin disease,						
CC	contact dermatitis, an allergic disease e.g. food hypersensitivity,						
CC	asthma, a transplantation associated disease, or a chronic inflammatory						
CC	demyelinating polynuropathy. Treating a degenerative cartilaginous						
CC	disorder comprises administering a PRO1031 or PRO1122 polypeptide						
CC	agonist, or antagonist to the mammal. Numerous examples of the diseases						
CC	and disorders are given in the specification						
XX							
XX	Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;						
SQ							

Db 1142 ATCATGAAATGTCGTCAGTGTTCGGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1201
QY 1293 TGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAGGCGAGAGAAATGGGTCA 1352
Db 1202 TGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAGGCGAGAGAAATGGGTCA 1261
QY 1353 TCCAGAACTCCAGAGTCCAGTTCATCATTTGTTGTTTTCCTCAAAAGGTATGAAGTACT 1412
Db 1262 TCCAGAACTCCAGAGTCCAGTTCATCATTTGTTGTTTTCCTCAAAAGGTATGAAGTACT 1321
QY 1413 TTGTGGACAAGAACTTACAAAACAAAGAGAGTGGCCGAGGCTCGGGGAAAAGAGAGC 1472
Db 1322 TTGTGGACAAGAACTTACAAAACAAAGAGAGTGGCCGAGGCTCGGGGAAAAGAGAGC 1381
QY 1473 TCTTCTGTTGGCGGTGTGAGCCTTGCCTGAAAGTCCGCGAGGCGCAAGCAGAGTTCGT 1532
Db 1382 TCTTCTGTTGGCGGTGTGAGCCTTGCCTGAAAGTCCGCGAGGCGCAAGCAGAGTTCGT 1441
QY 1533 CCGCGGCGCTCAGCAAGTTTATCGCGCTACTTTGATTATTCCTGCGAGGAGACGTCC 1592
Db 1442 CCGCGGCGCTCAGCAAGTTTATCGCGCTACTTTGATTATTCCTGCGAGGAGACGTCC 1501
QY 1593 CCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTT 1652
Db 1502 CCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTT 1561
QY 1653 CCCACTTGCATCCGAGACACAGGCTCTCAGAGCGGGGAGCAGCAGCGACAGGGCA 1712
Db 1562 CCCACTTGCATCCGAGACACAGGCTCTCAGAGCGGGGAGCAGCAGCGACAGGGCA 1621
QY 1713 GCAGAGAACTACTTCCGAGAGCAAGTCAGCGCGTCTATAGTCCGCAATTTGCAACA 1772
Db 1622 GCAGAGAACTACTTCCGAGAGCAAGTCAGCGCGTCTATAGTCCGCAATTTGCAACA 1681
QY 1773 TGCACCACTTATTTGACGAGGAGCCGACTGCTTCGAAAAGCAGTTCGTTCCCTTCCATC 1832
Db 1682 TGCACCACTTATTTGACGAGGAGCCGACTGCTTCGAAAAGCAGTTCGTTCCCTTCCATC 1741
QY 1833 CTCTCTCACTGGCTTACCGGAGGACAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1892
Db 1742 CTCTCTCACTGGCTTACCGGAGGACAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1801
QY 1893 ATGATGTCATGTGCAAAACAGGGCTGAGAGTCTCTGCTAAAGGTAGAGGGCGGTG 1952
Db 1802 ATGATGTCATGTGCAAAACAGGGCTGAGAGTCTCTGCTAAAGGTAGAGGGCGGTG 1861
QY 1953 TTCTTGGGGCAACCGGACCCGACTCCAGCAGAGAGTCCAGTTCGGGGCCCTGGACC 2012
Db 1862 TTCTTGGGGCAACCGGACCCGACTCCAGCAGAGAGTCCAGTTCGGGGCCCTGGACC 1921
QY 2013 AAGACGGGAGGCGCGGCTGCTTGAAGTTCGAGTTCGGGCGCTGCAACCCCTCTGTCACA 2072
Db 1922 AAGACGGGAGGCGCGGCTGCTTGAAGTTCGAGTTCGGGCGCTGCAACCCCTCTGTCACA 1981
QY 2073 CGGTGAAGCCGGAGCGGCTCGGACATGCGCGGAGCTCAGGCACTATGACTCGTCTG 2132
Db 1982 CGGTGAAGCCGGAGCGGCTCGGACATGCGCGGAGCTCAGGCACTATGACTCGTCTG 2041
QY 2133 TGCCCTCATCCGAGTGTCTCTGCACTGATGGAAGGACTCTCCGACGACAGACAGAGAA 2192
Db 2042 TGCCCTCATCCGAGTGTCTCTGCACTGATGGAAGGACTCTCCGACGACAGACAGAGAA 2101
QY 2193 CGTCTTCCCTGACGAGAGCGGTCTCTCTTTCAGGCTTGGGTGAGAGGAACTCTCTG 2252
Db 2102 CGTCTTCCCTGACGAGAGCGGTCTCTCTTTCAGGCTTGGGTGAGAGGAACTCTCTG 2161
QY 2253 CCCTTCTCTCAAGCTCTCTCTTCTGGTCTATGCAAGCAGATCTTGGTTCGCGCAGCT 2312
Db 2162 CCCTTCTCTCAAGCTCTCTCTTCTGGTCTATGCAAGCAGATCTTGGTTCGCGCAGCT 2221
QY 2313 ACACGTGATGAATCCACGCGGTGCGCCCTTCTGTAACAAAGAGAGTCTAAGCATTCG 2372

Db 2222 AACTGTATGAACCTCCACGCGGTGCGCCCTTTGTAAACAAAGAGTCTAAGCATTCG 2281
QY 2373 CACTTTA 2379
Db 2282 CACTTTA 2288
RESULT 10
ACA89858
ID ACA89858 standard; cDNA; 2319 BP.
XX ACA89858;
AC ACA89858;
XX 10-JUL-2003 (first entry)
XX Human cDNA encoding PRO20026.
XX Human; ss; gene; interleukin 17; IL-17; IL17 receptor; angiogenesis;
KW T-lymphocyte proliferation; inflammatory cell infiltration;
KW immune related disorder; systemic lupus erythematosus; osteoarthritis;
KW rheumatoid arthritis; spondyloarthritis; systemic sclerosis;
KW Sjogren's syndrome; sarcoidosis; autoimmune haemolytic anaemia;
KW thyroiditis; diabetes mellitus; immune-mediated renal disease;
KW demyelinating disease; Guillain-Barre syndrome; hepatobiliary disease;
KW hepatitis; inflammatory bowel disease; Whipple's disease; psoriasis;
KW immune-mediated skin disease; erythema multiforme; contact dermatitis;
KW allergic disease; asthma; atopic dermatitis; food hypersensitivity;
KW urticaria; immunologic disease of the lung; eosinophilic pneumonia;
KW idiopathic pulmonary fibrosis; transplantation associated disease;
KW graft-versus-host disease.
XX Homo sapiens.
OS US2003003546-A1.
PN 02-JAN-2003.
PD 22-MAR-2001; 2001US-00816744.
PF 15-MAY-1998; 98US-0085579P.
PX 23-DEC-1998; 98US-0113621P.
PR 08-MAR-1999; 99WO-US005028.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 09-JUN-1999; 99US-0138387P.
PR 23-DEC-1999; 99US-0172096P.
PR 30-DEC-1999; 99WO-US031274.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000WO-US007532.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-JUN-2000; 2000US-0213807P.
PR 24-AUG-2000; 2000WO-US023328.
PR 26-OCT-2000; 2000US-0242837P.
PR 26-OCT-2000; 2000US-0244072P.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
XX (GETH) GENENTECH INC.
XX Chen J, Filvaroff E, Pong S, Goddard A, Godowski P, Grimaldi C;
PI Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R;
PI Watanabe C, Williams PM, Wood WI, Yansura D;
XX

DR WPI: 2003-428843/40.
DR P-PSDB; ABU89705.
XX
PT New PRO polypeptides and polynucleotides homologous to interleukin-17,
PT useful for treating e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, or systemic
PT sclerosis.
XX
PS Claim 2; Fig 17; 129pp; English.
XX
CC The invention relates to a nucleic acid having similarity to interleukin-
CC 17 (IL-17) or IL-17 receptor comprises at least 80% nucleic acid sequence
CC identity to a nucleotide sequence which: (a) encodes a polypeptide having
CC a sequence of appearing as ABU89697-ABU89700 and ABU89702-ABU89705 (PI-
CC P8), lacking or having its associated signal peptide; (b) encodes an
CC extracellular domain of PI-P8 lacking its associated signal peptide; (c)
CC consists of a sequence of appearing as ACA89850-ACA89853 and ACA89855-
CC ACA8985687; or (d) consists of the full-length coding sequence of
CC selected from SI-S8, and of the cDNA deposited under ATCC accession
CC number 209866, 203552, PTA-1185, PTA-2108, PTA-202, PTA-1535, PTA-1082 or
CC PTA-2591. Also included are expression vectors, host cells, encoded
CC proteins, chimeric proteins, antibodies, ant/agonists, compounds
CC inhibiting the expression of SI-S8 or activity (or mimicking the activity
CC of) of PI-P8, stimulating/inhibiting the proliferation of T-lymphocytes
CC using the polypeptides or ant/agonists, enhancing the infiltration of
CC inflammatory cells into a tissue of a mammal by administering a PRO1031
CC polypeptide, its an agonist or antagonist, and inhibiting angiogenesis
CC induced by a PRO1031 polypeptide or its agonist in a mammal by
CC administering a PRO1031 polypeptide, its ant/agonist or an anti-PRO1031
CC antibody. The proteins, antibodies, ant/agonists and compounds are useful
CC for treating an immune related disorder such as systemic lupus
CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic
CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
CC thyroiditis, diabetes mellitus, immune-mediated renal disease, a
CC demyelinating disease of the central or peripheral nervous system,
CC chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes an IL17 or IL17
CC receptor homologue of the invention
XX
SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
Query Match 87.0%; Score 2074.2; DB 8; Length 2319;
Best Local Similarity 98.1%; Pred No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;
QY 252 AGGGAGTGGGGCCAGCCAGCAGAAACAGTGGGCTGTACAAATCAACCTTCAAAATATGACA 311
DB 122 AGGGAGTGGGGCCAGCCAGCAGAAACAGTGGGCTGTACAAATCAACCTTCAAAATATGACA 181
QY 312 ATTGTACACCTACTTGTGAATCAGTGGGAGCATGTGCTGACGCCGAGATATCA 371
DB 182 ATTGTACACCTACTTGTGAATCAGTGGGAGCATGTGCTGACGCCGAGATATCA 241
QY 372 CCATCAGCCAGTATCTTGTCCATGACCAAGTGGGAGTCAACCTTCTTTGGTCCCCAGGGG 431
DB 242 CCATCAGCCAGTATCTTGTCCATGACCAAGTGGGAGTCAACCTTCTTTGGTCCCCAGGGG 301
QY 432 CCCTCGGCATCGAATTCCTGAAAGGATTTCCGGGTAAATCTGAGGAGCTGAAGTCGGAGG 491
DB 302 CCCTCGGCATCGAATTCCTGAAAGGATTTCCGGGTAAATCTGAGGAGCTGAAGTCGGAGG 361

QY 492 GAAGACAGTGCACAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 551
DB 362 GAAGACAGTGCACAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 421
QY 552 GAACCTGGAATGGAATCTCAACCTTTCTGATATGAAATTTGAAACCGGATTTATTCGTAA 611
DB 422 GAACCTGGAATGGAATCTCAACCTTTCTGATATGAAATTTGAAACCGGATTTATTCGTAA 481
QY 612 AGGTGTGCTCCCTTTCTCCATTAATAAAGCAATTAACCACTTCTCTTTTAGAA 671
DB 482 AGGTGTGCTCCCTTTCTCCATTAATAAAGCAATTAACCACTTCTCTTTTAGAA 541
QY 672 CCCGAGCCTGTGACCTCTTGTTCAGCCGGAACAATCTAGCTTTGTAACCCCTTCTCGAAGC 731
DB 542 CCCGAGCCTGTGACCTCTTGTTCAGCCGGAACAATCTAGCTTTGTAACCCCTTCTCGAAGC 601
QY 732 CTGGAACCTGGAACATCAGCA----- 753
DB 602 CTGGAACCTGGAACATCAGCCAGCATGGCTCGGACATGCGAGGTGCTCTTCGACCAACGAC 661
QY 754 -GCATGGCTCGGACATGCGAGTGTCTTCGACCATGCGCCGACAACTTCGGCTTCGGTT 812
DB 662 CGCATGGCTCGGACATGCGAGTGTCTTCGACCATGCGCCGACAACTTCGGCTTCGGTT 721
QY 813 TCTTCTATCTTCACTACAAGCTCAAGCAACGAAGGACCTTTCAAGCGAAAGACCTGTGAAGC 872
DB 722 TCTTCTATCTTCACTACAAGCTCAAGCAACGAAGGACCTTTCAAGCGAAAGACCTGTGAAGC 781
QY 873 AGGAGCAAACTACAGAGCAACGACCTGCTCTTCAAAATGTTTCTCGAGGGGATATATA 932
DB 782 AGGAGCAAACTACAGAGCAACGACCTGCTCTTCAAAATGTTTCTCGAGGGGATATATA 841
QY 933 TAATTGAGCTGGTGATGACATTAACAACAAGAAAGTGAATGATTCATTCCTTAAAGC 992
DB 842 TAATTGAGCTGGTGATGACATTAACAACAAGAAAGTGAATGATTCATTCCTTAAAGC 901
QY 993 CAGTGCACTCCCGTGGGCGGCGCCATCAGAGCCGTGGCCATCAGAGTGCCTGGTAG 1052
DB 902 CAGTGCACTCCCGTGGGCGGCGCCATCAGAGCCGTGGCCATCAGAGTGCCTGGTAG 961
QY 1053 TCATATCGGATTCGCGACGCTCTTCACTGTGTGATGTCGCGCAAGCAACAAGAAATA 1112
DB 962 TCATATCGGATTCGCGACGCTCTTCACTGTGTGATGTCGCGCAAGCAACAAGAAATA 1021
QY 1113 TATATTCACATTTAGATGAGAGAGCTGTGCTCTCCACATACACTGCAGCACTCCCAA 1172
DB 1022 TATATTCACATTTAGATGAGAGAGCTGTGCTCTCCACATACACTGCAGCACTCCCAA 1081
QY 1173 GAGAGAGCTCCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1232
DB 1082 GAGAGAGCTCCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1141
QY 1233 ATCATCATGATGTCGTCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1292
DB 1142 ATCATCATGATGTCGTCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1201
QY 1293 TGGCTCTGGACCTGTGGGAGACTTTCAGCTCTGTAGAGAGGCGCAGAGAAATGGGTCA 1352
DB 1202 TGGCTCTGGACCTGTGGGAGACTTTCAGCTCTGTAGAGAGGCGCAGAGAAATGGGTCA 1261
QY 1353 TCCAGAGAGTCCAGAGTCCAGTTCATCTGTGTGTTTGTTCCTCAAGGATGATGATGACT 1412
DB 1262 TCCAGAGAGTCCAGAGTCCAGTTCATCTGTGTGTTTGTTCCTCAAGGATGATGATGACT 1321
QY 1413 TTGTGGCAAGAGAACTTACAAAACAAGAGAGTGGCCGAGGCTCGGGGAAAGAGAGC 1472
DB 1322 TTGTGGCAAGAGAACTTACAAAACAAGAGAGTGGCCGAGGCTCGGGGAAAGAGAGC 1381
QY 1473 TCTTCTGCTGGCGGTGTACGCCAATTCGCGAAAGCTCCGCGAGCCAGCAGAGTTCGT 1532
DB 1382 TCTTCTGCTGGCGGTGTACGCCAATTCGCGAAAGCTCCGCGAGCCAGCAGAGTTCGT 1441
QY 1533 CCGGGCGCTCAGCAAGTTTATCGCCGCTACTTTGATTTATTCCTGCGAGGAGACGTCC 1592

Db	1442	CCGCGGCGCTCAGCAAGTTTATCGCCCTCTACTTTGATTATTCTCTCGAGGGAGACGTCC	1501
Qy	1593	CCGGTATCTTAGACCTCAGTACCAAGTACAGACTCATGGACAATCTTCCCTCAGCTCTGTT	1652
Db	1502	CCGGTATCTTAGACCTCAGTACCAAGTACAGACTCATGGACAATCTTCCCTCAGCTCTGTT	1561
Qy	1653	CCCACTTGGCACTCCCGAGACCA CGGCCCTCAGGAGCCGGGGCAGCACACGCGACAGGGCA	1712
Db	1562	CCCACTTGCACTCCCGAGACCA CGGCCCTCAGGAGCCGGGGCAGCACACGCGACAGGGCA	1621
Qy	1713	GCAGAAGGAATCTACTTCCGAGCAAGTCAAGCCGGTCCCTATAGTTCGCCATTTGCNACA	1772
Db	1622	GCAGAAGGAATCTACTTCCGAGCAAGTCAAGCCGGTCCCTATAGTTCGCCATTTGCNACA	1681
Qy	1773	TGCACCAAGTTTATTGACGAGAGCCGCACTGGTTTCGAAAAGCAGTTTCGTTCCCTTCCATC	1832
Db	1682	TGCACCAAGTTTATTGACGAGAGCCGCACTGGTTTCGAAAAGCAGTTTCGTTCCCTTCCATC	1741
Qy	1833	CTCTCTCACTGCGCTACCGGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTTAA	1892
Db	1742	CTCTCTCACTGCGCTACCGGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTTAA	1801
Qy	1893	ATGATGTTCATGTGCAAAACGAGGCTCAGAGTGACTTCTCGCTTAAAGGTAGAGCGCGCTG	1952
Db	1802	ATGATGTTCATGTGCAAAACGAGGCTCAGAGTGACTTCTCGCTTAAAGGTAGAGCGCGCTG	1861
Qy	1953	TTCTTTGGGGCAACCGGACCAAGCGACTCCACGACAGAGAGTCAGCATGGGGGCTTGGACC	2012
Db	1862	TTCTTTGGGGCAACCGGACCAAGCGACTCCACGACAGAGAGTCAGCATGGGGGCTTGGACC	1921
Qy	2013	AAGACGGGGAGCCCGGCTTGCCTTTGACCGGTAGCGCGCGCTGCAACCCCTCTGTGCA	2072
Db	1922	AAGACGGGGAGCCCGGCTTGCCTTTGACCGGTAGCGCGCGCTGCAACCCCTCTGTGCA	1981
Qy	2073	CGGTGAAAGCGGGCAGCCCTCGACATGCGCGGGACTCAGGCATCTATGACTCTGCTG	2132
Db	1982	CGGTGAAAGCGGGCAGCCCTCGACATGCGCGGGACTCAGGCATCTATGACTCTGCTG	2041
Qy	2133	TGCCCTCATCCGAGCTGTCTCTGCGCACTGATGGAAGGACTCTCGACGGACCAAGAGAAA	2192
Db	2042	TGCCCTCATCCGAGCTGTCTCTGCGCACTGATGGAAGGACTCTCGACGGACCAAGAGAAA	2101
Qy	2193	CGTCTTCCCTGACGGAGAGGTGTCTCTCTTTCAGGCTGGGTGAGAGGAACCTCTCTG	2252
Db	2102	CGTCTTCCCTGACGGAGAGGTGTCTCTCTTTCAGGCTGGGTGAGAGGAACCTCTCTG	2161
Qy	2253	CCCTTCTCTTCCAAAGTCTCTCTTCTGGGTCAATGCAAGCAGATCTTGGTTTCGGCAGCT	2312
Db	2162	CCCTTCTCTTCCAAAGTCTCTCTTCTGGGTCAATGCAAGCAGATCTTGGTTTCGGCAGCT	2221
Qy	2313	ACACTGATGAATCTCAGCGGTTCGCCCTTTTGTAAACAAAACGAAAGAGTCTTAAGCATTCG	2372
Db	2222	ACACTGATGAATCTCAGCGGTTCGCCCTTTTGTAAACAAAACGAAAGAGTCTTAAGCATTCG	2281
Qy	2373	CACTTTAA 2379	
Db	2282	CACTTTAA 2288	

RESULT 11

RESOLUTION
ACA64642

ACA64642
ID ACA64642 standard; cDNA; 2319 BP.

XX
XX
DT
710704Z

ACA ACA64642;

XX
1860-1861

DT 17-JUN-2003 (first entry)

XX

DE Human cDNA encoding IL-17 family member, PRO20026.

XX XX

systemic sclerosis; idiopathic inflammatory myopathy; Sjögren's syndrome; sarcoidosis; rickets; rubeola; psoriasis; pernicious anaemia; pericarditis; diabetes mellitus; rheumatoid arthritis; active hepatitis; Guillain-Barré syndrome; inflammatory bowel disease; immune-mediated skin disease; contact dermatitis; allergic disease; asthma; urticaria; eosinophilic pneumonia; idiopathic pulmonary fibrosis; transplacental-associated disease; graft-versus-host disease.

Homo sapiens.

US2003008815-A1.

09-JAN-2003.

20-DEC-2000: 2000US-00747259.

14-MAY-1999. 99TTS-00311832

14-MAY-1999; 99US-0031183Z;
23-DEC-1999; 99US-0172096P;

23-DEC-1999; 99US-UI/2096F;
30-DEC-1999; 99WO-US031274.

30-DEC-1999; 99WO-US031274;
11-JAN-2000; 2000US-0175481P;

11-JAN-2000; 2000US-VI75481F.
18-FEB-2000; 2000WO-US004341.

18-FEB-2000; 2000WO-US0005841.
02-MAR-2000; 2000WO-US0005841.

21-MAR-2000; 2000US-0191007P.

21-MAR-2000; 2000WO-US007532.

02-JUN-2000; 2000WO-US015264.

20-JUN-2000; 2000US-0213087P.

22-AUG-2000; 2000US-00644848.

24-AUG-2000; 2000WO-US023328.

24-OCT-2000; 2000US-0242837P.

10-NOV-2000; 2000WO-US030873.

28-NOV-2000; 2000US-0253646P.

01-DEC-2000; 2000WO-US032678.

(GETH) GENENTECH INC.

Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi C;

Gurney AL, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R;

Watanabe C, Williams PM, Wood WI, Yansura DG;

WPI; 2003-341350/32.

P-PSDB; ABU72600.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1031, PRO1122, PRO10272, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2: Fig 17: 148pp: English.

The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to 8 cDNA sequences encoding PRO polypeptides (or their extracellular domains) which are members of the interleukin-17 (IL-17) family of cytokines. Also included are expression vectors, host cells, the PRO polypeptides, chimaeric molecules comprising the above polypeptides fused to a heterologous amino acid sequence, an anti-PRO antibody, a composition comprising the above polypeptide, (or its agonist or antagonist, or the antibody cited above) in combination with a carrier, determining the presence of a PRO polypeptide in a sample, identifying a compound that mimics or inhibits the activity of the polypeptides cited above, or a compound that inhibits the expression of a gene encoding the above polypeptides, stimulating or inhibiting the proliferation of T-lymphocytes, enhancing or decreasing the infiltration of inflammatory cells into a tissue of a mammal and inhibiting or stimulating angiogenesis induced by a PRO1031 polypeptide or its agonist in a mammal. The nucleic acid is useful in molecular biology, e.g. use as a hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptide or the antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, and in various diagnostic assays. For immune-related disorders,

these may be systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin disease, bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, immunologic disease of the lung, eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, transplantation-associated disease, graft rejection or graft-versus-host disease. The composition is useful in treating the above-mentioned immune-related diseases in a mammal, or in increasing or inhibiting the proliferation of T-lymphocytes, or increasing or decreasing the infiltration of inflammatory cells into a tissue of a mammal. The present sequence encodes a PRO polypeptide of the invention

xx
SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;

Query Match 87.0%; Score 2074.2; DB 8; Length 2319;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;

QY 252 AGGGAGTGGGCGCAGCCAGCAGAGAACAGTGGGCTGTACAAATCACCTTCAAAATATGACA 311
DB 122 AGGGAGTGGGCGCAGCCAGCAGAACAGTGGGCTGTACAAATCACCTTCAAAATATGACA 181
QY 312 ATTGTACCACTACTTGAATCAGTGGGGAAGCATGTGATGCTGACGCCCAGCAATATCA 371
DB 182 ATTGTACCACCTACTTGAATCAGTGGGGAAGCATGTGATGCTGACGCCCAGCAATATCA 241
QY 372 CCATCAGCAGTATGCTTGGCATGACCAAGTGGGAGTCACCATCTTTGGTCCCCAGGG 431
DB 242 CCATCAGCAGTATGCTTGGCATGACCAAGTGGGAGTCACCATCTTTGGTCCCCAGGG 301
QY 432 CCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGGAGAGCTGAAGTCGGAGG 491
DB 302 CCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGGAGAGCTGAAGTCGGAGG 361
QY 492 GAAGACAGTGCACCAACTGATTTCTAAAGGATTCGAAGCAGCTCAACAGTAGCTTCAAAA 551
DB 362 GAAGACAGTGCACCAACTGATTTCTAAAGGATTCGAAGCAGCTCAACAGTAGCTTCAAAA 421
QY 552 GAACTGGAATGGAAATCTCAACTTTCTGAAATATGAATTTGAAACGGATTTATTCGTA 611
DB 422 GAACTGGAATGGAAATCTCAACTTTCTGAAATATGAATTTGAAACGGATTTATTCGTA 481
QY 612 AGTTGTCCCTTTCTTCCATTAATAACGAAAGCAATACCACTTTCTTTCTTTAGAA 671
DB 482 AGTTGTCCCTTTCTTCCATTAATAACGAAAGCAATACCACTTTCTTTCTTTAGAA 541
QY 672 CCGAGCCTGTGACTGTGTGTGTACAGCCGGACAATCTAGCTTTGTAACCCCTTCTGGAAGC 731
DB 542 CCGAGCCTGTGACTGTGTGTGTGTACAGCCGGACAATCTAGCTTTGTAACCCCTTCTGGAAGC 601
QY 732 CTCGGAACTGAACTCAGCCCA----- 753
DB 602 CTCGGAACTGAACTCAGCCCAAGCATGCTCGGACATGCGAGGTGCTTCGACACCGCAC 661
QY 754 -GCATGGCTCGGACATGCAAGTGTCTTTCGACCATGCAACCACTTCGGCTTCCGTT 812
DB 662 GCATGGCTCGGACATGCAAGTGTCTTTCGACCATGCAACCACTTCGGCTTCCGTT 721
QY 813 TCTTCTATCTTCACTACAGCTCAAGAGGACCTTTCAAGGAAAGACCTGTGAAGC 872
DB 722 TCTTCTATCTTCACTACAGCTCAAGAGGACCTTTCAAGGAAAGACCTGTGAAGC 781

QY 873 AGGAGCAAACTACAGAGACGACCAAGCTGCCTCTTCAAAATGTTTCTCCAGGGGATTAATA 932
DB 782 AGGAGCAAACTACAGAGATGACGAGCTGCCTCTTCAAAATGTTTCTCCAGGGGATTAATA 841
QY 933 TAATTGAGCTGGTGGATGACACTAAACAACAAGAAAGATGATGATATATGCTTAAAGC 992
DB 842 TAATTGAGCTGGTGGATGACACTAAACAACAAGAAAGATGATGATATATGCTTAAAGC 901
QY 993 CAGTGCACTCCCGTGGGCGGCCCATCAGAGCCGTGGCCATCACAAGTGCACCTGGTAG 1052
DB 902 CAGTGCACTCCCGTGGGCGGCCCATCAGAGCCGTGGCCATCACAAGTGCACCTGGTAG 961
QY 1053 TCATATCGCATTCGCGACGCTCTTCACTGTGATGTGCCGCAAGAACACAAGAAATA 1112
DB 962 TCATATCGCATTCGCGACGCTCTTCACTGTGATGTGCCGCAAGAACACAAGAAATA 1021
QY 1113 TATATTCACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA 1172
DB 1022 TATATTCACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA 1081
QY 1173 GAGAGAGCTCCGCGCGGCCGGAAGTCTTCTCTGCTATTTCCAGTAAAGATGGCCAGA 1232
DB 1082 GAGAGAGCTCCGCGCGGCCGGAAGTCTTCTCTGCTATTTCCAGTAAAGATGGCCAGA 1141
QY 1233 ATCATGAAATGTGCTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1292
DB 1142 ATCATGAAATGTGCTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1201
QY 1293 TGGCTCTGGAGCTGTGGGAAGACTTTCAGCCCTCTGTAGAGAGGCGCAGAGAAATGGGTCA 1352
DB 1202 TGGCTCTGGAGCTGTGGGAAGACTTTCAGCCCTCTGTAGAGAGGCGCAGAGAAATGGGTCA 1261
QY 1353 TCCAGAGAGTCCAGAGTCCCAGTTCATCTGTTGTTTGTTCGAAAGGTATGAAGTACT 1412
DB 1262 TCCAGAGAGTCCAGAGTCCCAGTTCATCTGTTGTTTGTTCGAAAGGTATGAAGTACT 1321
QY 1413 TTGTGGCAAGAGAACTCAAAACAAGAGAGTGGCCGAGGCTCGGGGAAAGAGAGC 1472
DB 1322 TTGTGGCAAGAGAACTCAAAACAAGAGAGTGGCCGAGGCTCGGGGAAAGAGAGC 1381
QY 1473 TCTTCTGTGGTGGCGGTGTAGCCATTTCCGAAAGCTCCGCGAGGCCCAAGCAGAGTTCGT 1532
DB 1382 TCTTCTGTGGTGGCGGTGTAGCCATTTCCGAAAGCTCCGCGAGGCCCAAGCAGAGTTCGT 1441
QY 1533 CCGCGGCGCTCAGCAAGTTTATCGCGCTCTACTTTGATTTATTTCTGCGAGGAGACGTCC 1592
DB 1442 CCGCGGCGCTCAGCAAGTTTATCGCGCTCTACTTTGATTTATTTCTGCGAGGAGACGTCC 1501
QY 1593 CCGGTATCTAGACCTCAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTT 1652
DB 1502 CCGGTATCTAGACCTCAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTT 1561
QY 1653 CCCACTTGCACCTCCGAGACCAAGCGCTCCAGAGCGCGGGCAGCACAAGCAGAGGGCA 1712
DB 1562 CCCACTTGCACCTCCGAGACCAAGCGCTCCAGAGCGCGGGCAGCACAAGCAGAGGGCA 1621
QY 1713 GCAGAAGCACTCTTCGGAGCAAGTCCAGCCGCTCCCTATACGTGCGCAATTTGCAACA 1772
DB 1622 GCAGAAGCACTCTTCGGAGCAAGTCCAGCCGCTCCCTATACGTGCGCAATTTGCAACA 1681
QY 1773 TGCAACCACTTTATTTGACGAGGAGCCGAGCTGGTTTCGAAAGCAGTTCGTTCCCTTCCATC 1832
DB 1682 TGCAACCACTTTATTTGACGAGGAGCCGAGCTGGTTTCGAAAGCAGTTCGTTCCCTTCCATC 1741
QY 1833 CTCCTCACTCGGCTACCGGGAGCAGTCTTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1892
DB 1742 CTCCTCACTCGGCTACCGGGAGCAGTCTTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1801
QY 1893 ATGATGTCACTGTCAAAACAGGGCTGAGAGTGAATCTCTGCTAAAGGTAGAGCGGCTG 1952
DB 1802 ATGATGTCACTGTCAAAACAGGGCTGAGAGTGAATCTCTGCTAAAGGTAGAGCGGCTG 1861
QY 1953 TTCTTGGGGCAACCGGACCCAGCCGACTCCAGCAGCAGAGGTTCAGCATGGGGGCTTGGACC 2012

```
Db 1862 TTCTGGGGCAACCGGACAGCCGACTCCAGCACGAGAGTCAGCATGGGGGCTGGACC 1921
Qy 2013 AAGACGGGGGCGCGGCTGCTTGGAGCGGTAGCGCGCCCTGCAACCCCTGCTGCACA 2072
Db 1922 AAGACGGGGGCGCGGCTGCTTGGAGCGGTAGCGCGCCCTGCAACCCCTGCTGCACA 1981
Qy 2073 CGGTGAAGCGGGACCGCCCTCGACATGCGCGGGACTCAGGCATCTATGACTCGTCTG 2132
Db 1982 CGGTGAAGCGGGACCGCCCTCGACATGCGCGGGACTCAGGCATCTATGACTCGTCTG 2041
Qy 2133 TGCCCTCATCCGAGTGTCTTGCACATGATGGAAGGACTCTCGACGACACAGAGAAA 2192
Db 2042 TGCCCTCATCCGAGTGTCTTGCACATGATGGAAGGACTCTCGACGACACAGAGAAA 2101
Qy 2193 CGTCTTCCCTGACGGAGAGCGTGTCTCTTTCAGGCTGGTGAGGAGAACTCTCTG 2252
Db 2102 CGTCTTCCCTGACGGAGAGCGTGTCTCTTTCAGGCTGGTGAGGAGAACTCTCTG 2161
Qy 2253 CCCTTCCCTTCAAGCTCTCTCTTCTGGGTATGCAAAAGCAGATCTTGGTTGCCGCGAGCT 2312
Db 2162 CCCTTCCCTTCAAGCTCTCTCTTCTGGGTATGCAAAAGCAGATCTTGGTTGCCGCGAGCT 2221
Qy 2313 ACATGATGAATCCACGCGGTGCGCCCTTTGTAAACAAAACGAAAGACTCTAAGCATTGC 2372
Db 2222 ACATGATGAATCCACGCGGTGCGCCCTTTGTAAACAAAACGAAAGACTCTAAGCATTGC 2281
Qy 2373 CACTTTA 2379
Db 2282 CACTTTA 2288

RESULT 12
ID ADA43240 standard; cDNA; 2319 BP.
AC
XX ADA43240;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human interleukin 17 related mammalian cytokine polypeptide cDNA #9.
XX
XX ss; Gene; interleukin 17; cytokine; IL-17E; immune-related disease;
XX inflammatory disease; psoriasis; asthma; allergic rhinitis;
XX rheumatoid arthritis; human; interleukin 17 related mammalian cytokine.
XX
XX Homo sapiens.
XX
XX US6579520-B2.
XX
XX 17-JUN-2003.
XX
XX 22-MAR-2001; 2001US-00816744.
XX
XX 15-MAY-1998; 98US-0085579P.
XX
XX 23-DEC-1998; 98US-0113621P.
XX
XX 21-APR-1999; 99US-0130232P.
XX
XX 26-APR-1999; 99US-0131022P.
XX
XX 14-MAY-1999; 99US-00311832.
XX
XX 14-MAY-1999; 99US-0134287P.
XX
XX 09-JUN-1999; 99US-0138387P.
XX
XX 23-DEC-1998; 99US-0172096P.
XX
XX 11-JAN-2000; 2000US-0175481P.
XX
XX 21-MAR-2000; 2000US-0191007P.
XX
XX 22-JUN-2000; 2000US-0213807P.
XX
XX 24-OCT-2000; 2000US-0242837P.
XX
XX 26-OCT-2000; 2000US-0244072P.
XX
XX 28-NOV-2000; 2000US-0253646P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski P, Grimaldi C;
XX Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R;
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PI Watanabe C, Williams PM, Wood WI, Yansura D;
XX WPI; 2003-615512/58.
DR P-PSDB; ADA43241.
XX
XX New interleukin 17 related mammalian cytokine polypeptide (IL-17E)
PI polypeptide, useful for preparing composition for treating immune-related
PT or inflammatory diseases, e.g. psoriasis, asthma, allergic rhinitis or
PT rheumatoid arthritis.
XX
XX Example 8; Fig 17; 235pp; English.
PS
XX The invention relates to a new isolated interleukin 17 related mammalian
CC cytokine polypeptide (IL-17E). The polypeptide is useful for preparing a
CC composition for treating immune-related or inflammatory diseases, e.g.
CC psoriasis, asthma, allergic rhinitis or rheumatoid arthritis. The present
CC sequence represents cDNA encoding a human interleukin 17 related
CC mammalian cytokine polypeptide.
XX
SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;

Query Match 87.0%; Score 2074.2; DB 9; Length 2319;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;

Qy 252 AGGAGTGGGCGCCAGCAGCAAGTGGCTGTACACATCACCTTCAAAATATGACA 311
Db 122 AGGAGTGGGCGCCAGCAGCAAGTGGCTGTACACATCACCTTCAAAATATGACA 181
Qy 312 ATTGTACACCTACTTGAATCCAGTGGGAAGCATGTGTTCTGACGCCCGCATATCA 371
Db 182 ATTGTACACCTACTTGAATCCAGTGGGAAGCATGTGTTCTGACGCCCGCATATCA 241
Qy 372 CCATCAGCCAGTGTCTTGCCATGACCAAGTGGCAGTCACCATCTTTGGTCCCAGGG 431
Db 242 CCATCAGCCAGTGTCTTGCCATGACCAAGTGGCAGTCACCATCTTTGGTCCCAGGG 301
Qy 432 CCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTAAATCTCGAGGAGCTGAAGTCGGAGG 491
Db 302 CCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTAAATCTCGAGGAGCTGAAGTCGGAGG 361
Qy 492 GAAGACAGTGCCCAACACTGATTTCTAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAA 551
Db 362 GAAGACAGTGCCCAACACTGATTTCTAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAA 421
Qy 552 GAACTGGAATCGAATCTCAACCTTTCTCTGAATATGAAATTTGAAACGAGTATTTCGTAA 611
Db 422 GAACTGGAATCGAATCTCAACCTTTCTCTGAATATGAAATTTGAAACGAGTATTTCGTAA 481
Qy 612 AGGTTGTCCCTTTTCTTCCATTAAACGAAAGCAATTACCACCTTTCTTTTAGAA 671
Db 482 AGGTTGTCCCTTTTCTTCCATTAAACGAAAGCAATTACCACCTTTCTTTTAGAA 541
Qy 672 CCCGAGCCTGTGACCTGTGTGTATACGCCGGAATCTAGCTTGTAAACCTTCTCGAAGC 731
Db 542 CCCGAGCCTGTGACCTGTGTGTATACGCCGGAATCTAGCTTGTAAACCTTCTCGAAGC 601
Qy 732 CTGCGAAGCTGAAATCAGCCA----- 753
Db 602 CTGCGAAGCTGAAATCAGCCA----- 661
Qy 754 -GCATGGCTCGGACATGCAAGGTGTCTTTCGACCATGCAACCGCAACTTCGGCTTCGGTT 812
Db 662 CGCATGGCTCGGACATGCAAGGTGTCTTTCGACCATGCAACCGCAACTTCGGCTTCGGTT 721
Qy 813 TCTTCTATCTTCACTAAGCTCAAGCAGGAGCCTTTCAGCGAAGACCTGTAGC 872
Db 722 TCTTCTATCTTCACTAAGCTCAAGCAGGAGCCTTTCAGCGAAGACCTGTAGC 781
Qy 873 AGGACCAACTACAGAGACCGACCTGCTCCCTTCAAAATGTTTCTCCAGGGGATTATA 932
Db 782 AGGACCAACTACAGAGATGACCGCTGCTCCCTTCAAAATGTTTCTCCAGGGGATTATA 841
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QY 933 TAAATTGAGCTGGTGGATGACACTAACACAACAAGAAAGTATGATTTATGCTTAAAGC 992
Db 842 TAAATTGAGCTGGTGGATGACACTAACACAACAAGAAAGTATGATTTATGCTTAAAGC 901
QY 993 CAGTGCACTCCCGGTGGGCGCGGCCCATCAGAGCGGTGGCCCATCACAGTGCCACTGGTAG 1052
Db 902 CAGTGCACTCCCGGTGGGCGCGGCCCATCAGAGCGGTGGCCCATCACAGTGCCACTGGTAG 961
QY 1053 TCATATCGGCAATTCGCGACGCTCTTCACTGTGTATGTGCGGCAAGAGCAACAAGAAATA 1112
Db 962 TCATATCGGCAATTCGCGACGCTCTTCACTGTGTATGTGCGGCAAGAGCAACAAGAAATA 1021
QY 1113 TATATTACATTTAGATCAAGAGAGCTCTGAGTCTTCCACATACACTCCAGCACTCCCAA 1172
Db 1022 TATATTACATTTAGATCAAGAGAGCTCTGAGTCTTCCACATACACTCCAGCACTCCCAA 1081
QY 1173 GAGAGAGCTCCGGCGCGGCCGGAAGGTCTTTCTGCTATTTCAGTAAAGATGGCCAGA 1232
Db 1082 GAGAGAGCTCCGGCGCGGCCGGAAGGTCTTTCTGCTATTTCAGTAAAGATGGCCAGA 1141
QY 1233 ATCATGAATGTGCTCAGTGTGTTGCGCTACTTCTCCAGAGCTTCTGTGGCTGTGAGG 1292
Db 1142 ATCATGAATGTGCTCAGTGTGTTGCGCTACTTCTCCAGAGCTTCTGTGGCTGTGAGG 1201
QY 1293 TGGCTCTGCACTGTGGCAAGACTTTCAGCCTCTGTAGAGAGGGCAGAGAAATGGGTCA 1352
Db 1202 TGGCTCTGCACTGTGGCAAGACTTTCAGCCTCTGTAGAGAGGGCAGAGAAATGGGTCA 1261
QY 1353 TCCAGAAGATCCAGAGTCCAGTTCATCATTTGTTGTTTTCAGAGGTATGAAGTACT 1412
Db 1262 TCCAGAAGATCCAGAGTCCAGTTCATCATTTGTTGTTTTCAGAGGTATGAAGTACT 1321
QY 1413 TTGTGGACAAGAGAACTACAAAACAAGAGAGTGGCCGAGGCTCGGGGAAAGAGAGC 1472
Db 1322 TTGTGGACAAGAGAACTACAAAACAAGAGAGTGGCCGAGGCTCGGGGAAAGAGAGC 1381
QY 1473 TCTTCTGCTGGCGGTGTCAGCAATGCGCAAGAGTCCGCGAGCCAGCAGAGTTGCT 1532
Db 1382 TCTTCTGCTGGCGGTGTCAGCAATGCGCAAGAGTCCGCGAGCCAGCAGAGTTGCT 1441
QY 1533 CCGGGCGCTCAGCAAGTTTATCGCGTCTACTTTGATTATTTCTTCGAGGAGACGTCC 1592
Db 1442 CCGGGCGCTCAGCAAGTTTATCGCGTCTACTTTGATTATTTCTTCGAGGAGAGCTCC 1501
QY 1593 CCGGTATCCTAGACTGATGATCAAGTACAGACTCATGACAAATCTTCTCAGCTCTGTT 1652
Db 1502 CCGGTATCCTAGACTGATGATCAAGTACAGACTCATGACAAATCTTCTCAGCTCTGTT 1561
QY 1653 CCCACTTGCATCCCGAGACCAAGCCCTCCAGGAGCCGGGCGAGCACACGCGAGGGCA 1712
Db 1562 CCCACTTGCATCCCGAGACCAAGCCCTCCAGGAGCCGGGCGAGCACACGCGAGGGCA 1621
QY 1713 GCAGAAGAACTACTTTCGGAGCAAGTCAAGCCGCTCCCTATACGTCGCCATTTGCAACA 1772
Db 1622 GCAGAAGAACTACTTTCGGAGCAAGTCAAGCCGCTCCCTATACGTCGCCATTTGCAACA 1681
QY 1773 TGCACAGTTATTTGAGAGAGGAGCCGAGCTGTGTTGAAAAGCAGTTGTTCCCTCCATC 1832
Db 1682 TGCACAGTTATTTGAGAGAGGAGCCGAGCTGTGTTGAAAAGCAGTTGTTCCCTCCATC 1741
QY 1833 CTCCTCCACTGGCTTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1892
Db 1742 CTCCTCCACTGGCTTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1801
QY 1893 ATGATGTATGTGCAAAACAGGGCTGAGAGTGAATTTCTGCTTAAAGGTAGAGCGGCTG 1952
Db 1802 ATGATGTATGTGCAAAACAGGGCTGAGAGTGAATTTCTGCTTAAAGGTAGAGCGGCTG 1861
QY 1953 TTCTTTGGGCAACCGGACAGCCGACTCCAGACACAGAGTCAGATCGGGGCTGGACC 2012
Db 1862 TTCTTTGGGCAACCGGACAGCCGACTCCAGACACAGAGTCAGATCGGGGCTGGACC 1921
QY 2013 AAGACGGGAGGCGCGGCTGCGCTTGACGGTGTAGCGCGCCCTGCAACCCCTGCTGCACA 2072

Db 1922 AAGACGGGAGGCGCGGCTGCGCTTGACGGTGTAGCGCGCCCTGCAACCCCTGCTGCACA 1981
QY 2073 CGGTGAAAGCGGCGAGCCCTCGGACATGCGCGGGGACTCAGGCATCTATGACTCGTCTG 2132
Db 1982 CGGTGAAAGCGGCGAGCCCTCGGACATGCGCGGGGACTCAGGCATCTATGACTCGTCTG 2041
QY 2133 TGGCCTCATCCGAGCTCTCTGCGCACTGTATGGAAGGACTCTCGACGGACCCAGACAGAAA 2192
Db 2042 TGGCCTCATCCGAGCTCTCTGCGCACTGTATGGAAGGACTCTCGACGGACCCAGACAGAAA 2101
QY 2193 CGTCTTCCCTGACGAGAGCGGTGTCTCTCTTTCAGGCTCGGGTGAGGAGAACTCCTG 2252
Db 2102 CGTCTTCCCTGACGAGAGCGGTGTCTCTCTTTCAGGCTCGGGTGAGGAGAACTCCTG 2161
QY 2253 CCCTTCTTCCAGAGCTCTCTCTTTCGGGTGATGCAAGAGAGTCTTGGTTGCCGAGCT 2312
Db 2162 CCCTTCTTCCAGAGCTCTCTCTTTCGGGTGATGCAAGAGAGTCTTGGTTGCCGAGCT 2221
QY 2313 ACCTGTGTAAGTCCAGCGGTGCGCCCTTGTAAACAAAACGAAAGAGTCTAAGCATTTGC 2372
Db 2222 ACCTGTGTAAGTCCAGCGGTGCGCCCTTGTAAACAAAACGAAAGAGTCTAAGCATTTGC 2281
QY 2373 CACTTTA 2379
Db 2282 CACTTTA 2288
RESULT 13
ADA49781
ID ADA49781 standard; cDNA; 2319 BP.
XX
AC ADA49781;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human interleukin-17/interleukin-17 receptor related PRO20026 cDNA.
XX
KW Human; interleukin-17; IL-17; gene; ss; dermatological;
KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
KW osteopathic; antianaemic; antidiabetic; antithyroid; haemostatic;
KW hepatotropic; antipsoriatic; antiallergic; antiasthmatic; vasotropic;
KW gene therapy; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW spondyloarthropathy; systemic sclerosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome;
KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
KW immune-mediated renal disease; demyelinating disease;
KW Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;
KW hepatitis; primary biliary cirrhosis; sclerosing cholangitis;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW Whipple's disease; skin disease; erythema multiforme; contact dermatitis;
KW psoriasis; allergic disease; asthma; allergic rhinitis;
KW atopic dermatitis; food hypersensitivity; urticaria;
KW eosinophilic pneumonia; idiopathic pulmonary fibrosis;
KW hypersensitivity pneumonitis; transplantation; graft rejection;
KW graft-versus-host-disease.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 70..2256
FT /*tag= a
FT /product= "PRO20026"
FT /note= "Interleukin-17 and interleukin-17 receptor
FT related protein"
XX
XX US2002177188-A1.
XX PN
XX PD 28-NOV-2002.
XX

PF 05-JUN-2001; 2001US-00874503.
 XX 15-MAY-1998; 98US-0085579P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 21-APR-1999; 99US-0130232P.
 PR 26-APR-1999; 99US-0131022P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 14-MAY-1999; 99WO-US010733.
 PR 09-JUN-1999; 99US-0138387P.
 PR 23-DEC-1999; 99US-0172096P.
 PR 30-DEC-1999; 99WO-US031274.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 22-JUN-2000; 2000US-0213807P.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 24-OCT-2000; 2000US-0242837P.
 PR 26-OCT-2000; 2000US-0244072P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.

(GETH) GENENTECH INC.

XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi JC;
 PI Gurney A, Li H, Hillan K, Hymowitz SG, Tumas D, Starovozasnik MA;
 PI Lookeren WV, Vandlen R, Watanabe C, Williams PM, Wood W;
 PI Yansura DG;

XX WPI: 2003-605676/57.
 DR P-PSDB; ADA49782.

XX Novel polypeptides having sequence similarity to interleukin-17 and
 PT interleukin-17 receptor protein useful for treating, diagnosing immune
 PT related disorders and treating degenerative cartilaginous disorder in a
 PT mammal.

XX Claim 130; Fig 17; 140pp; English.

XX The invention describes an isolated polypeptide (I) having at least 80%
 CC amino acid sequence identity to interleukin(IL)-17 and IL-17 receptor
 CC protein. The novel PRO polypeptides are useful for treating an immune
 CC related disorder such as systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis,
 CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory
 CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis,
 CC diabetes mellitus, immune-mediated renal disease, demyelinating disease
 CC of the central or peripheral nervous system, idiopathic demyelinating
 CC polynuropathy, Guillain-Barre syndrome, chronic inflammatory
 CC demyelinating polynuropathy, hepatobiliary disease, infectious or
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis,
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
 CC disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or
 CC immune-mediated skin disease, bullous skin disease, erythema multiforme,
 CC contact dermatitis, psoriasis, allergic disease, asthma, allergic
 CC rhinitis, atopic dermatitis, food hypersensitivity, urticaria,
 CC immunologic disease of the lung, eosinophilic pneumonia, idiopathic
 CC pulmonary fibrosis, hypersensitivity pneumonitis, transplantation
 CC associated disease or graft rejection or graft-versus-host-disease, in a
 CC mammal. An anti-(I)-antibody is useful for determining the presence of
 CC PRO polypeptide in a sample suspected of containing the polypeptide and
 CC for diagnosing an immune related disease in a mammal. (I) is useful for
 CC identifying a compound that inhibits the activity of PRO polypeptide or
 CC expression of gene encoding PRO polypeptide, by contacting cells which
 CC normally express the polypeptide with a candidate compound, and

CC determining the lack of responsiveness by the cell or expression of the
 CC gene. This sequence encodes a novel PRO polypeptide with sequence
 CC similarity to interleukin-17 and the interleukin-17 receptor.

XX Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;

Query Match 87.0%; Score 2074.2; DB 9; Length 2319;
 Best Local Similarity 98.1%; Pred. No. 0;
 Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;

QY 252 AGGAGTGGGCCAGCAGCAAGAAACAGTGGCGTGTACAAATCACCCTTCAAAATATGACA 311
 DB 122 AGGAGTGGGCCAGCAGCAAGAAACAGTGGCGTGTACAAATCACCCTTCAAAATATGACA 181
 QY 312 ATTGTACCACTTCTGAATCCAGTGGGAAAGCATGTGATTGCTGACGCCAGAAATATCA 371
 DB 182 ATTGTACCACTTCTGAATCCAGTGGGAAAGCATGTGATTGCTGACGCCAGAAATATCA 241
 QY 372 CCATCAGCCAGTATGCTTGCATGACCAAGTGGGAGTCAACATTCCTTTGGTCCCAGGGG 431
 DB 242 CCATCAGCCAGTATGCTTGCATGACCAAGTGGGAGTCAACATTCCTTTGGTCCCAGGGG 301
 QY 432 CCCTGGCATCGAATTCCTGAAAGGATTTCCGGGTAATACTGAGGAGCTGAAGTCGGAGG 491
 DB 302 CCCTGGCATCGAATTCCTGAAAGGATTTCCGGGTAATACTGAGGAGCTGAAGTCGGAGG 361
 QY 492 GAAGACAGTGCACCAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 551
 DB 362 GAAGACAGTGCACCAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 421
 QY 552 GAACCTGGAATGGAATCTCAACCTTTCTGTAATATGAAATTTGAAACGGATATTTTCGTAA 611
 DB 422 GAACCTGGAATGGAATCTCAACCTTTCTGTAATATGAAATTTGAAACGGATATTTTCGTAA 481
 QY 612 AGTTGTCCCTTTCTTCCATTAAGAAAGCAAGCAATTAACCCCTTCTCTTTAGAA 671
 DB 482 AGTTGTCCCTTTCTTCCATTAAGAAAGCAAGCAATTAACCCCTTCTCTTTAGAA 541
 QY 672 CCCGAGCTGTGACCTGTGTTTACAGCCGACAACTTAGCTTTGTAACCCCTTCTCGAAGC 731
 DB 542 CCCGAGCTGTGACCTGTGTTTACAGCCGACAACTTAGCTTTGTAACCCCTTCTCGAAGC 601
 QY 732 CTCGAACTCTCAACATCAGCCA ----- 753
 DB 602 CTCGAACTCTCAACATCAGCCAAGTGTGCTTCGACCAAGCAGC 661
 QY 754 -GCATGGCTCGGACATGACAGTGTCTTCGACCATGACCCGACAACTTCGGCTTCGGTT 812
 DB 662 CGCATGGCTCGGACATGACAGTGTCTTCGACCATGACCCGACAACTTCGGCTTCGGTT 721
 QY 813 TCTTCTATCTTCACTACAGAGCTCAAGCAGCAAGGACCTTTCAAGCGAAAGACCTGTAGC 872
 DB 722 TCTTCTATCTTCACTACAGAGCTCAAGCAGCAAGGACCTTTCAAGCGAAAGACCTGTAGC 781
 QY 873 AGGCAAACTACAGAGACGACCTGCTCTCTTCAAAATGTTTCTCCAGGGATATA 932
 DB 782 AGGCAAACTACAGAGATGACCACTGCTCTCTTCAAAATGTTTCTCCAGGGATATA 841
 QY 933 TAAATGAGCTGGTGAATGACACTAAACAAGAAAGTGTATGATATGCTTAAAGC 992
 DB 842 TAAATGAGCTGGTGAATGACACTAAACAAGAAAGTGTATGATATGCTTAAAGC 901
 QY 993 CAGTGCATCTCCCGTGGGCGGCGCCATCAGAGCGCTGCGCCATCAGTGCACCTGGTAG 1052
 DB 902 CAGTGCATCTCCCGTGGGCGGCGCCATCAGAGCGCTGCGCCATCAGTGCACCTGGTAG 961
 QY 1053 TCATATCGCATTCGCGACGCTCTTCTCACTGTGATGTGCGCAAGCAAGCAAGAAATA 1112
 DB 962 TCATATCGCATTCGCGACGCTCTTCTCACTGTGATGTGCGCAAGCAAGCAAGAAATA 1021
 QY 1113 TATATTCATTTAGATGAAGAGAGCTGTAGCTTCTTCCATACACTGACGACTCCCAA 1172
 DB 1022 TATATTCATTTAGATGAAGAGAGCTGTAGCTTCTTCCATACACTGACGACTCCCAA 1081

PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
XX (GETH) GENENTECH INC.
XX
XX Chen J, Filvaroff E, Fong S, French D, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Hillan KJ, Hymowitz SG, Li H, Pan J;
PI Starovaenik MA, Tumas D, Van Lookeren M, Vandlen R, Watanabe CK;
PI Williams PM, Wood WI, Yaneura DG;
XX
DR WPI; 2003-605678/57.
DR P-PSDB; ADA26975.
XX
XX New isolated IL-17 nucleic acids and polypeptides, useful for diagnosing
PT and treating disorders with aberrant expression or activity of the IL-17
PT polypeptide, such as degenerative cartilaginous and immune-related
PT disorders.
XX
XX Claim 2; Fig 17; 161pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The novel
CC PRO polypeptides are human interleukin 17 (hIL-17) homologues. The PRO
CC polypeptide and polynucleotide sequences are useful for diagnosing and
CC treating disorders associated with the aberrant expression or activity of
CC a PRO polypeptide. The disorders include degenerative cartilaginous
CC disorders and immune related diseases, such as systemic lupus
CC erythematosus (SLE), rheumatoid arthritis, osteoarthritis, juvenile
CC inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, an idiopathic
CC chronic arthritis, spondyloarthropathy, autoimmune thrombocytopaenia,
CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,
CC thyroiditis, diabetes mellitus, immune-mediated renal disease, a
CC demyelinating disease of the central or peripheral nervous system,
CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a
CC chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation-associated disease, graft rejection or
CC graft-versus-host-disease. The present sequence encodes a human PRO
XX polypeptide of the invention.
XX
SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;

Query Match 87.0%; Score 2074.2; DB 9; Length 2319;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;
QY 252 AGGAGTGGGGCAGCAGGAGAAACAGTGGGCTGTACACATCACCTTCATATATGACA 311
DB 122 AGGAGTGGGGCAGCAGGAGAAACAGTGGGCTGTACACATCACCTTCATATATGACA 181
QY 312 ATTGTACCACTACTTGAATCCAGTGGGAAGCATGTGTTGCTGACGCCCAATATCA 371

DB 182 ATTGTACCACTACTTGAATCCAGTGGGGAAGCATGTGTTGCTGACGCCCAATATCA 241
QY 372 CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGGAGTCAACATTTCTTTGGTCCCAGGG 431
DB 242 CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGGAGTCAACATTTCTTTGGTCCCAGGG 301
QY 432 CCCTCGGCATCGAATTTCTGAAAGGATTTCCGGTAAATCTGAGGAGCTGAAGTCGGAGG 491
DB 302 CCCTCGGCATCGAATTTCTGAAAGGATTTCCGGTAAATCTGAGGAGCTGAAGTCGGAGG 361
QY 492 GAAGCAGTGGCAACAACTGATTTCTAAAGGATCGAAGCAGCTCAACAGTAGCTTCAAAA 551
DB 362 GAAGCAGTGGCAACAACTGATTTCTAAAGGATCGAAGCAGCTCAACAGTAGCTTCAAAA 421
QY 552 GAACTGGAATGGAATCTCAACCTTTCTCTGAATATGAAATTTGAAACGGATATTTTCGTA 611
DB 422 GAACTGGAATGGAATCTCAACCTTTCTCTGAATATGAAATTTGAAACGGATATTTTCGTA 481
QY 612 AGTTTGTCCCTTTCTCTCAATTAAGGATTTTACCAACCTTTCTCTTTAGAA 671
DB 482 AGTTTGTCCCTTTCTCTCAATTAAGGATTTTACCAACCTTTCTCTTTAGAA 541
QY 672 CCGGAGCCTGTGACCTGTGTTTACAGCCGGAATCTAGCTTGTAAACCTTCTCGAAGC 731
DB 542 CCGGAGCCTGTGACCTGTGTTTACAGCCGGAATCTAGCTTGTAAACCTTCTCGAAGC 601
QY 732 CTGGAACCTGAAACATCAGCCA----- 753
DB 602 CTGGAACCTGAAACATCAGCCAGCATGGCTCGGACATGCAGTGTCTTCGACCAAGC 661
QY 754 -GCATGGCTCGGACATGCAAGTGTCTTTCGACCATGCAACCTTCGCTTCGCTT 812
DB 662 CGCATGGCTCGGACATGCAAGTGTCTTTCGACCATGCAACCTTCGCTTCGCTT 721
QY 813 TCTTTCTATCTCACTCAAGCTCAAGCAGGAGGACCTTCAAGCGAAGACCTCTGAAGC 872
DB 722 TCTTTCTATCTCACTCAAGCTCAAGCAGGAGGACCTTCAAGCGAAGACCTCTGAAGC 781
QY 873 AGGACCAACTACAGAGCAGCAGCTGCTCTCTTCAAAATGTTTCTCCAGGGGATTATA 932
DB 782 AGGACCAACTACAGAGATGACAGCTGCTCTCTTCAAAATGTTTCTCCAGGGGATTATA 841
QY 933 TAAATTGAGCTGGTGGATGACACTAACCAAGAAAAAGTGTATGCTTAAAGC 992
DB 842 TAAATTGAGCTGGTGGATGACACTAACCAAGAAAAAGTGTATGCTTAAAGC 901
QY 993 CAGTGCACCTCCCGTGGGCGGCGCCATCAGAGCGTGGCCATCAGTGGCCACTGGTAG 1052
DB 902 CAGTGCACCTCCCGTGGGCGGCGCCATCAGAGCGTGGCCATCAGTGGCCACTGGTAG 961
QY 1053 TCATATCGGCATTTCCGCGACGCTCTTCACTGTGTATGTCGCGCAAGCAAGCAAGAAATA 1112
DB 962 TCATATCGGCATTTCCGCGACGCTCTTCACTGTGTATGTCGCGCAAGCAAGCAAGAAATA 1021
QY 1113 TATATTTCATTTAGATGAAGAGAGCTGTAGTCTTCCACATACACTGCAGCAGCTCCCAA 1172
DB 1022 TATATTTCATTTAGATGAAGAGAGCTGTAGTCTTCCACATACACTGCAGCAGCTCCCAA 1081
QY 1173 GAGAGAGCTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1232
DB 1082 GAGAGAGCTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1141
QY 1233 ATCATATGAATGCTGTCAGTGTCTTTCGCTACTTCTCTCAGGACCTTCTGTGGCTGTGAGG 1292
DB 1142 ATCATATGAATGCTGTCAGTGTCTTTCGCTACTTCTCTCAGGACCTTCTGTGGCTGTGAGG 1201
QY 1293 TGGCTCTGGACCTGTGGGAAGACTTTCAGCTCTGTAGAGAGGGGCGGAGAGAGATGGGTCA 1352
DB 1202 TGGCTCTGGACCTGTGGGAAGACTTTCAGCTCTGTAGAGAGGGGCGGAGAGAGATGGGTCA 1261
QY 1353 TCCAGAGATCCACGAGTCCCAAGTTCATATTTGTGGTGTGTTTCCAAAGGTATGAAGTACT 1412
DB 1262 TCCAGAGATCCACGAGTCCCAAGTTCATATTTGTGGTGTGTTTCCAAAGGTATGAAGTACT 1321

PT sclerosis.
XX Claim 2; Fig 17; 154pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequence encoding them. The novel
CC PRO polypeptides show sequence similarity to interleukin-17 (IL-17) and
CC to the IL-17 receptor. The PRO polypeptides, agonists, antagonists and
CC antibodies that specifically bind to the PRO polypeptides are useful for
CC treating an immune related disorder in a mammal, such as systemic lupus
CC erythematosus (SLE), rheumatoid arthritis, osteoarthritis, juvenile
CC chronic arthritis, spondyloarthritis, systemic sclerosis, idiopathic
CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC sarcoidosis, autoimmune hemolytic anaemia, diabetes mellitus, immune-
CC mediated renal disease, demyelinating disease of the central or
CC peripheral nervous system, Guillain-Barre syndrome, hepatobiliary
CC disease, immune-mediated skin disease, food hypersensitivity, urticaria,
CC or graft-versus-host disease. A composition comprising a PRO polypeptide,
CC agonist, antagonist or antibody is useful for the treatment of an immune
CC related disease in a mammal and is capable of increasing or inhibiting
CC the proliferation of T-lymphocytes in, or increasing or decreasing
CC infiltration of inflammatory cells into a tissue. The present sequence
CC encodes a human PRO polypeptide of the invention.
XX
SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
Query Match 87.0%; Score 2074.2; DB 10; Length 2319;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;
QY 252 AGGGAGTGGGCGAGCAGCAAAACAGTGGGCTGTACAAATACACCTTCAATATGACA 311
DB 122 AGGGAGTGGGCGAGCAGCAAAACAGTGGGCTGTACAAATACACCTTCAATATGACA 181
QY 312 ATTTGACCACTTCTGAATCAGTGGGAAGCATGTGATGCTGACGCCCAAGATATCA 371
DB 182 ATTTGACCACTTCTGAATCAGTGGGAAGCATGTGATGCTGACGCCCAAGATATCA 241
QY 372 CCATCAGCCAGTATGCTTCCATGACCAAGTGGGAGTCAACATCTTTGGTCCCGAGGG 431
DB 242 CCATCAGCCAGTATGCTTCCATGACCAAGTGGGAGTCAACATCTTTGGTCCCGAGGG 301
QY 432 CCTCGGCATGAAATCTCTGAAAGGATTTCCGGTAAATCTCAGGAGCTGAAAGTCCGAGG 491
DB 302 CCTCGGCATGAAATCTCTGAAAGGATTTCCGGTAAATCTCAGGAGCTGAAAGTCCGAGG 361
QY 492 GAAGACAGTCCCAACCACTGATTTAAAGGATCCGAAGCAGCTCAACAGTACTTCAAAA 551
DB 362 GAAGACAGTCCCAACCACTGATTTAAAGGATCCGAAGCAGCTCAACAGTACTTCAAAA 421
QY 552 GAATGGAAATGAAATCTCAACCTTCTGAAATATGAAATTTGAAACGGATATTTCTGTA 611
DB 422 GAATGGAAATGAAATCTCAACCTTCTGAAATATGAAATTTGAAACGGATATTTCTGTA 481
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DB 482 AGTTGTCCTTTCTTCCATTAATAAGCAATTTACCACTTTCTTTTAGAA 541
QY 672 CCGGAGCCTGTGACCTGTTGTTACAGCCGGAATCTAGCTTTGTAACCTTTCTGGAAGC 731
DB 542 CCGGAGCCTGTGACCTGTTGTTACAGCCGGAATCTAGCTTTGTAACCTTTCTGGAAGC 601
QY 732 CTGCGAATCTGAACATCAGCCA----- 753
DB 602 CTGCGAATCTGAACATCAGCCAGCATGGCTCGGACATGCGAGTGTCTTTCGACCAAGC 661
QY 754 -GCATGGCTCGACATGAGTGTCTTCCGACCATCGCAGCACTTTCGGCTTCGGTT 812
DB 662 CGCATGGCTCGACATGAGTGTCTTCCGACCATCGCAGCACTTTCGGCTTCGGTT 721
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DB 1082 GAGAGAGCTCCGCGCGCGCGGAGGCTTCTCTGCTATTCCAGTAAAGATGCCAGA 1141
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DB 1322 TTGTGGAACAAGAAGAACTACAAACAACAAGAGAGTGGCGAGGTCGGGGAAAGAGAGC 1381
QY 1473 TCTTCTCGTGGCGGTGTGAGCATTGCGGAAAGCTCGCCAGCCGAGCAGAGTTCGT 1532
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DB 1442 CCGGCGCTCAGCAAGTTTATCGCGCTACTTTGATTATTCCTGCGAGGAGAGCTCC 1501
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QY 1653 CCCACTTCACCTCCGAGACCAAGCTCCAGAGCCGCGGGCAGACAGCCGAGAGGCA 1712
DB 1562 CCCACTTCACCTCCGAGACCAAGCTCCAGAGCCGCGGGCAGACAGCCGAGAGGCA 1621
QY 1713 GCAGAAGAACTACTTCCGAGCAAGTCAAGCCGCTCCCTATACCTGCGCATTTGCAACA 1772
DB 1622 GCAGAAGAACTACTTCCGAGCAAGTCAAGCCGCTCCCTATACCTGCGCATTTGCAACA 1681
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DB 1682 TGCACAGTTTATTCAGAGGAGCCGAGTGTGTTGAAAAGCAGTTCGTTCCCTTCCATC 1741
QY 1833 CTCCTCCATGCGCTACCGGAGCCAGTCTTCGAGAAATTTGATTCGGGCTTGGTTTTAA 1892
DB 1742 CTCCTCCATGCGCTACCGGAGCCAGTCTTCGAGAAATTTGATTCGGGCTTGGTTTTAA 1801
QY 1893 ATGATGTCTATGTGCAAAACGAGGCTGAGAGTGAATTCGCTCAAGGTAGAGGGCGGCTG 1952
DB 1802 ATGATGTCTATGTGCAAAACGAGGCTGAGAGTGAATTCGCTCAAGGTAGAGGGCGGCTG 1861

Qy	1953	TTCTTGGGCAACCGGACAGCGACTCCAGACAGAGAGTCAAGATGGGGGCTTGACCC	2012
Db	1862	TTTTTGGGGCAACCGGACAGCGACTCCAGACAGAGAGTCAAGATGGGGGCTTGACCC	1921
Qy	2013	AAGACGGGGAGCGCGGCTGCTCCCTTGACGGTAGCGCGCCCTGCAACCCCTGCTGCACA	2072
Db	1922	AAGACGGGGAGCGCGGCTGCTCCCTTGACGGTAGCGCGCCCTGCAACCCCTGCTGCACA	1981
Qy	2073	CGGTGAAGCGGGAGCGCGGCTGCGACATGCCCGGGACTCAGGCATCTATGACTCGTCTG	2132
Db	1982	CGGTGAAGCGGGAGCGCGGCTGCGACATGCCCGGGACTCAGGCATCTATGACTCGTCTG	2041
Qy	2133	TGCCCTCATCCGAGCTGCTCTGCCACTGATGGAAGGACTCTCGACGGACCCAGACAGAAA	2192
Db	2042	TGCCCTCATCCGAGCTGCTCTGCCACTGATGGAAGGACTCTCGACGGACCCAGACAGAAA	2101
Qy	2193	CGTCTTCCCTGACGGAGAGCGTGTCTCTTTCAGGCTTGGGTGAGGAGGAACCTCCTG	2252
Db	2102	CGTCTTCCCTGACGGAGAGCGTGTCTCTTTCAGGCTTGGGTGAGGAGGAACCTCCTG	2161
Qy	2253	CCCTTCCCTTCCAAGTCTCTCTTCTGGGTGATGCAAGCAGATCTTGGTTGCCGCGAGCT	2312
Db	2162	CCCTTCCCTTCCAAGTCTCTCTTCTGGGTGATGCAAGCAGATCTTGGTTGCCGCGAGCT	2221
Qy	2313	ACACTGATGAATCCACGCGGTGCGCCCTTTGTAAACAAAACGAAAGAGTCTAAGCATTGC	2372
Db	2222	ACACTGATGAATCCACGCGGTGCGCCCTTTGTAAACAAAACGAAAGAGTCTAAGCATTGC	2281
Qy	2373	CACTTTA	2379
Db	2282	CACTTTA	2288

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Job time : 1373.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2005, 00:22:23 ; Search time 420.208 Seconds
(without alignments)
9279.331 Million cell updates/sec

Title: US-10-717-282-1
Perfect score: 2383
Sequence: 1 ccgcgcgcgcacccacccac.....aagcattgccacttagctg 2383

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2074.2	87.0	2319	4	US-09-747-259-17
2	1873	78.6	3948	4	US-09-799-451-125
3	71.4	3.0	3223	2	US-08-620-694A-9
4	71.4	3.0	3223	3	US-09-022-255-9
5	71.4	3.0	3223	3	US-09-022-696-9
6	71.4	3.0	3223	3	US-08-978-773-3
7	71.4	3.0	3223	3	US-09-022-253-9
8	71.4	3.0	3223	3	US-09-022-260-9
9	71.4	3.0	3223	3	US-09-022-259-9
10	71.4	3.0	3223	3	US-09-022-257-9
11	71.4	3.0	3223	4	US-09-549-679-9
12	54.6	2.3	3288	2	US-08-620-694A-1
13	54.6	2.3	3288	3	US-09-022-255-1
14	54.6	2.3	3288	3	US-09-022-696-1
15	54.6	2.3	3288	3	US-08-978-773-1
16	54.6	2.3	3288	3	US-09-022-253-1
17	54.6	2.3	3288	3	US-09-022-260-1
18	54.6	2.3	3288	3	US-09-022-259-1
19	54.6	2.3	3288	3	US-09-022-257-1
20	54.6	2.3	3288	4	US-09-549-679-1
21	45.2	1.9	72704	4	US-09-902-540-1273
22	42.8	1.8	1263	4	US-09-724-797-94
23	42.6	1.8	601	4	US-09-949-016-200159
24	42.6	1.8	111509	4	US-09-949-016-17379
25	42.4	1.8	1137	4	US-09-902-540-8621
26	42.4	1.8	7982	4	US-09-902-540-911
27	42.2	1.8	288	4	US-09-489-039A-3694

ALIGNMENTS

RESULT 1

US-09-747-259-17

Sequence 17, Application US/09747259

Patent No. 6569645

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Chen, Jian

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Li, Hanzhong

APPLICANT: Hillan, Kenneth

APPLICANT: Tumas, Daniel

APPLICANT: VanLookeren, Menno

APPLICANT: Vanden, Richard

APPLICANT: Watanabe, Colin

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William

APPLICANT: Yansura, Daniel

TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

FILE REFERENCE: P1381R1C1F1 (US)

CURRENT APPLICATION NUMBER: US/09747,259

CURRENT FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: US 09/311,832

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: US 60/172,096

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: PCT/US99/31274

PRIOR FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: US 60/175,481

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/US00/04341

PRIOR FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 60/191,007

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: PCT/US00/07532

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: PCT/US00/15264

PRIOR FILING DATE: 2000-06-02

PRIOR APPLICATION NUMBER: US 60/213,087

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: US 09/844,848

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24

Sequence 3665, Ap
Sequence 3882, Ap
Sequence 2359, Ap
Sequence 1875, Ap
Sequence 857, Ap
Sequence 45, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 10393, A
Sequence 10765, A
Sequence 10280, A
Sequence 10680, A
Sequence 36, Appl
Sequence 5, Appl
Sequence 19, Appl
Sequence 1, Appl

;; PRIOR APPLICATION NUMBER: US 60/242,837
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: US 60/253,646
;; PRIOR FILING DATE: 2000-11-28
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 17
;; LENGTH: 2319
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-747-259-17

Query Match 87.0%; Score 2074.2; DB 4; Length 2319;

Best Local Similarity 98.1%; Pred. No. 0;

Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;

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QY	312	ATTGTACCACTACTTTGAATCAGTGGGCAAGCATGTATTGCTGACGCCCAGAAATATCA	371
DB	182	ATTGTACCACTACTTTGAATCAGTGGGCAAGCATGTATTGCTGACGCCCAGAAATATCA	241
QY	372	CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGCAGTCACCATTTCTTTGGTCCCGAGGG	431
DB	242	CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGCAGTCACCATTTCTTTGGTCCCGAGGG	301
QY	432	CCCTCGGCATCGAATCTCTGAAGGATTTCCGGTAATCTGAGGAGCTGAAGTCGGAGG	491
DB	302	CCCTCGGCATCGAATCTCTGAAGGATTTCCGGTAATCTGAGGAGCTGAAGTCGGAGG	361
QY	492	GAAGACAGTGCACCAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA	551
DB	362	GAAGACAGTGCACCAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA	421
QY	552	GAATGGGAATGGAATCTCAACTCTTCTGAATATGAAATTTGAAACGGATATTTCGTAA	611
DB	422	GAATGGGAATGGAATCTCAACTCTTCTGAATATGAAATTTGAAACGGATATTTCGTAA	481
QY	612	AGTTTGCTCCCTTTCTTCCATTAATAAAGCAATTTACACCCCTTCTCTTTAGAA	671
DB	482	AGTTTGCTCCCTTTCTTCCATTAATAAAGCAATTTACACCCCTTCTCTTTAGAA	541
QY	672	CCCGAGCCTGTGACCTGTGTTTACAGCCGGAACAATCTAGCTTTGTAACCCCTTCTGGAAGC	731
DB	542	CCCGAGCCTGTGACCTGTGTTTACAGCCGGAACAATCTAGCTTTGTAACCCCTTCTGGAAGC	601
QY	732	CTCGGAACCTGAAACATCAGCCA-----	753
DB	602	CTCGGAACCTGAAACATCAGCCAGCATGCTCGGACATGCGTGTCTTCGACACCGCAC	661
QY	754	-GCATGGCTCGGAACATGCAAGTGTCTTCGACCAATGCAACCGGCAAACTTCGGCTTCGGTT	812
DB	662	CGCATGGCTCGGAACATGCAAGTGTCTTCGACCAATGCAACCGGCAAACTTCGGCTTCGGTT	721
QY	813	TCTTCTATCTTCACTTACAGCTCAAGCAGCAAGGACCTTTCAAGCGAAAGACCTGTAAAGC	872
DB	722	TCTTCTATCTTCACTTACAGCTCAAGCAGCAAGGACCTTTCAAGCGAAAGACCTGTAAAGC	781
QY	873	AGGAGCAAACTACAGAGCAGCAGCTGCTCTCTTCAAAATGTTTCTCAGGGGATTATA	932
DB	782	AGGAGCAAACTACAGAGCAGCAGCTGCTCTCTTCAAAATGTTTCTCAGGGGATTATA	841
QY	933	TAAATTGAGCTGGTGATGACACTAACAACAAGAAAGATGATGATATGCTTTAAAGC	992
DB	842	TAAATTGAGCTGGTGATGACACTAACAACAAGAAAGATGATGATATGCTTTAAAGC	901
QY	993	CAGTGCACTCCCGTGGGCGGGCCCATCAGAGCCGTGGCCATCAGAGTGCACCTGGTAG	1052

DB	902	CAGTGCACTCCCGTGGGCGGGCCCATCAGAGCCGTGGCCCATCACAGTGCACCTGGTAG	961
QY	1053	TCATATCGGCATTTCCGCAACGCTCTTCACTGTGATGTCGCCAAGCAACAAGAAATA	1112
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QY	1113	TATATTCACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA	1172
DB	1022	TATATTCACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA	1081
QY	1173	GAGAGAGCTCCGCGCCGCGCGGAAGTCTTCTCTGCTATTCCAGTAAAGATGCCAGA	1232
DB	1082	GAGAGAGCTCCGCGCCGCGCGGAAGTCTTCTCTGCTATTCCAGTAAAGATGCCAGA	1141
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QY	1353	TCCAGAGAGATCCAGAGTCCCAGTTCATCATTTGTGTTTGTTCAAAAGGTATGAAGTACT	1412
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QY	1413	TTGTGGACAAGAGAACTACAAACAAGAGAGTGGCCGAGGCTCGGGGAAAGAGAGGC	1472
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QY	1473	TCCTTCTGTGGGCTGTGAGCCATTCGCGAAAGCTCCGCGAGGCGCAAGCAGAGTTTCTG	1532
DB	1382	TCCTTCTGTGGGCTGTGAGCCATTCGCGAAAGCTCCGCGAGGCGCAAGCAGAGTTTCTG	1441
QY	1533	CCGCGGCGCTCAGCAAGTTTATCCGCGTCTACTTTGATTATTCTCGAGGAGACGCTCC	1592
DB	1442	CCGCGGCGCTCAGCAAGTTTATCCGCGTCTACTTTGATTATTCTCGAGGAGACGCTCC	1501
QY	1593	CCGCTATCTTAGACTGAGTACCAAGTACAGATCATGGAACAATCTTCTCAGCTCTGTT	1652
DB	1502	CCGCTATCTTAGACTGAGTACCAAGTACAGATCATGGAACAATCTTCTCAGCTCTGTT	1561
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DB	1562	CCCACTTGCACTCCGAGACCAAGGCTCCAGGAGCCGGGCGCAGCACACGCGCAGAGGCA	1621
QY	1713	GCAGAGGAATCTCTCCGAGCAAGTCAGGCGGTCCTCTATACGTGCGCAATTTGCAACA	1772
DB	1622	GCAGAGGAATCTCTCCGAGCAAGTCAGGCGGTCCTCTATACGTGCGCAATTTGCAACA	1681
QY	1773	TGCAACAGTTTATGACAGAGAGCCGACTGGTTTCGAAAGCAGTTCGTTCCCTTCATC	1832
DB	1682	TGCAACAGTTTATGACAGAGAGCCGACTGGTTTCGAAAGCAGTTCGTTCCCTTCATC	1741
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DB	1742	CTCTCTCACTCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA	1801
QY	1893	ATGATGTCAATGTGCAAAACACAGGCGCTCAGAGTGAATCTCTGCTTAAAGGTAGAGCGGCTG	1952
DB	1802	ATGATGTCAATGTGCAAAACACAGGCGCTCAGAGTGAATCTCTGCTTAAAGGTAGAGCGGCTG	1861
QY	1953	TTCTTTGGGCAACCGGACCAAGCCGACTCCAGCAAGAGAGTCAAGTGGGGGCTTGAGCC	2012
DB	1862	TTCTTTGGGCAACCGGACCAAGCCGACTCCAGCAAGAGAGTCAAGTGGGGGCTTGAGCC	1921
QY	2013	AAGACGGGAGGCGCGGCTTCCCTTCAAGTACGCGCCCTCGAACCCCTGCTGCACA	2072
DB	1922	AAGACGGGAGGCGCGGCTTCCCTTCAAGTACGCGCCCTCGAACCCCTGCTGCACA	1981
QY	2073	CGGTGAAAGCGGCGAGCCCTTCGACATGCGCGGGAGCTCAGGGCATCTATGACTCGTCTG	2132
DB	1982	CGGTGAAAGCGGCGAGCCCTTCGACATGCGCGGGAGCTCAGGGCATCTATGACTCGTCTG	2041

QY 2133 TGCCCTCATCCGAGCTGTCTCTGCACTGATGAAGGACTCTCGACGACAGACAGAAA 2192
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QY 2193 CGCTTCCTTGACGAGAGCGGTGCTCTCTTTCAGGGCTGGGTGAGAGAACTCTCTG 2252
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US-09-799-451-125

; Sequence 125, Application US/09799451

; Patent No. 6783959

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

; APPLICANT: Zhang, Jie

; APPLICANT: Xue, Aidong J.

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Ma, Yunding

; APPLICANT: Yamazaki, Victoria

; APPLICANT: Chen, Rui-hong

; APPLICANT: Wang, Zhiwei

; APPLICANT: Wang, Dunrui

; APPLICANT: Yang, Yonghong

; APPLICANT: Wehrman, Tom

; APPLICANT: Ghosh, Reena

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6783959el Nucleic Acids and

; FILE REFERENCE: Polypeptides

; CURRENT APPLICATION NUMBER: US/09/799,451

; CURRENT FILING DATE: 2001-03-05

; NUMBER OF SEQ ID NOS: 948

; SOFTWARE: pt_FL_genes Version 2.0

; SEQ ID NO 125

; LENGTH: 3948

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (60)..(1844)

US-09-799-451-125

Query Match 78.6%; Score 1873; DB 4; Length 3948;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1876; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 503 CAACAACTGATTTAAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAAAGAACTGGAATG 562
DB 3 CAACAACTGATTTAAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAAAGAACTGGAATG 62
QY 563 GAATCTCAACCTTCTGTAATATGAAATTTGAAAACGGATATTTTGTAAAGGTTGTCCCT 622
DB 63 GAATCTCAACCTTCTGTAATATGAAATTTGAAAACGGATATTTTGTAAAGGTTGTCCCT 122

QY 623 TTTCTTCCATTAATAAAGCAATTAACAACCTTTCTTTCTTTAGAACCGAGCCTGT 682
DB 123 TTTCTTCCATTAATAAAGCAATTAACAACCTTTCTTTCTTTAGAACCGAGCCTGT 182
QY 683 GACCTGTGTTTACAGCGGCAATCTAGCTTGTAAACCTTTCTGGAACCTTCGGAACCTG 742
DB 183 GACCTGTGTTTACAGCGGCAATCTAGCTTGTAAACCTTTCTGGAACCTTCGGAACCTG 242
QY 743 AACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTCGACCATGCAACCGACAATTC 802
DB 243 AACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTCGACCATGCAACCGACAATTC 302
QY 803 GGCCTCCGTTTCTTCTATCTTACTACAACTCAAGCTCAAGCAGGAGCCTTTCAAGCGAAG 862
DB 303 GGCCTCCGTTTCTTCTATCTTACTACAACTCAAGCTCAAGCAGGAGCCTTTCAAGCGAAG 362
QY 863 ACCTGTAAGCAGGAGCAAACTACAGACGACGCTGCTCTTCAAAAATGTTTCTCCA 922
DB 363 ACCTGTAAGCAGGAGCAAACTACAGACGATGACGCTGCTCTTCAAAAATGTTTCTCCA 422
QY 923 GGGGATTAATAATTAGCTGGTGGATGACACTAAACAACAAGAAAAGTGATGATTAAT 982
DB 423 GGGGATTAATAATTAGCTGGTGGATGACACTAAACAACAAGAAAAGTGATGATTAAT 482
QY 983 GCCTTAAAGCCAGTGCACTCCCGTGGGCGGCGCCCATCAGAGCGTGCCCATCAAGTG 1042
DB 483 GCCTTAAAGCCAGTGCACTCCCGTGGGCGGCGCCCATCAGAGCGTGCCCATCAAGTG 542
QY 1043 CCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCGCGAAGAGCAA 1102
DB 543 CCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCGCGAAGAGCAA 602
QY 1103 CAAGAAAATATATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCA 1162
DB 603 CAAGAAAATATATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCA 662
QY 1163 GCATCTCCAAAGAGAGAGCTCCGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1222
DB 663 GCATCTCCAAAGAGAGAGCTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 722
QY 1223 GATGCCAGAGATCACATGAATGTCGTCAGTGTTCGCTACTTCTCCAGACACTTCTGT 1282
DB 723 GATGCCAGAGATCACATGAATGTCGTCAGTGTTCGCTACTTCTCCAGACACTTCTGT 782
QY 1283 GGCTGTAGGTGGCTCTGCACTCTGGGAAGACTTTCAGCCTCTGTAGAGAGGGCAGAGA 1342
DB 783 GGCTGTAGGTGGCTCTGCACTCTGGGAAGACTTTCAGCCTCTGTAGAGAGGGCAGAGA 842
QY 1343 GAATGGGTCAATCCAGAGATCCAGATCCAGTTCATCATGTGGTGTTCCTTCCAAAGGT 1402
DB 843 GAATGGGTCAATCCAGAGATCCAGATCCAGTTCATCATGTGGTGTTCCTTCCAAAGGT 902
QY 1403 ATGAAGTACTTGTGGCAAGAGACTTACAAACAAGAGGAGTGGCGGCGGCGGCGGCGG 1462
DB 903 ATGAAGTACTTGTGGCAAGAGACTTACAAACAAGAGGAGTGGCGGCGGCGGCGGCGG 962
QY 1463 AAAGGAGAGCTCTTCTCGTGGCGGTGTCAGCCTTTCGGAAGAAAGCTCCGCGAGGCCAAG 1522
DB 963 AAAGGAGAGCTCTTCTCGTGGCGGTGTCAGCCTTTCGGAAGAAAGCTCCGCGAGGCCAAG 1022
QY 1523 CAGAGTCTCGTCCGCGGCGCTCAGCAAGTTTATCGCGTCTACTTTGATTTATTCCTGCGAG 1582
DB 1023 CAGAGTCTCGTCCGCGGCGCTCAGCAAGTTTATCGCGTCTACTTTGATTTATTCCTGCGAG 1082
QY 1583 GGAGAGCTCCCGGTATCTAGACTGATGATGATGATGATGATGATGATGATGATGATGATG 1642
DB 1083 GGAGAGCTCCCGGTATCTAGACTGATGATGATGATGATGATGATGATGATGATGATGATG 1142
QY 1643 CAGCTCTGTCTCCACTTCCAGTCCCGAGACCAAGCCTCCAGAGCGCGGCGGCGGCGGCGG 1702
DB 1143 CAGCTCTGTCTCCACTTCCAGTCCCGAGACCAAGCCTCCAGAGCGCGGCGGCGGCGGCGG 1202
QY 1703 CGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1762

1203 CGACAGGCGCAGAGGAACTACTTCGGAGCAAGTCCAGCGCGTCCCTATAGTCGCC 1262
1763 ATTTCGAATGACACAGTATTTATGACAGAGAGCCCGACTGGTTCGAAAAGAGTTCGTT 1822
1263 ATTTCGAATGACACAGTATTTATGACAGAGAGCCCGACTGGTTCGAAAAGAGTTCGTT 1322
1823 CCGTTCATCTCTCCCTCACTGGCTACCGGAGAGCCAGTTCGGAGAAATTTGATTTCGGGC 1882
1323 CCGTTCATCTCTCCCTCACTGGCTACCGGAGAGCCAGTTCGGAGAAATTTGATTTCGGGC 1382
1883 TTGTTTAAATGATGTCATGTCGAAAACAGGCGCTGAGAGTGAATTCGCTTAAAGTA 1942
1383 TTGTTTAAATGATGTCATGTCGAAAACAGGCGCTGAGAGTGAATTCGCTTAAAGTA 1442
1943 GAGCGGCTGTTCTTGGGGCAACCGGACACGCGGACTCCAGACGAGAGTCAAGTGGG 2002
1443 GAGCGGCTGTTCTTGGGGCAACCGGACACGCGGACTCCAGACGAGAGTCAAGTGGG 1502
2003 GGCTGGACACAGAGCGGAGCGCGGCTGCGCTTGAAGTGGAGCGCGCTGCAACCC 2062
1503 GGCTGGACACAGAGCGGAGCGCGGCTGCGCTTGAAGTGGAGCGCGCTGCAACCC 1562
2063 CTGCTGCACACGTTGAAAGCGGACGCGGCTCGGACATGCGCGGACTCAGGCACTTAT 2122
1563 CTGCTGCACACGTTGAAAGCGGACGCGGCTCGGACATGCGCGGACTCAGGCACTTAT 1622
2123 GACTGCTGTCGCTCATGTCGAGAGTGTCTGCGACATGTCGCAAGGACTCTGACGGAC 2182
1623 GACTGCTGTCGCTCATGTCGAGAGTGTCTGCGACATGTCGCAAGGACTCTGACGGAC 1682
2183 CAGACAGAAAGCTCTTCCCTGACGAGAGCGTGTCTCTTCAAGGCTGGGTGAGGAG 2242
1683 CAGACAGAAAGCTCTTCCCTGACGAGAGCGTGTCTCTTCAAGGCTGGGTGAGGAG 1742
2243 GAACCTCTGCGCTTCTTCAAGTCTCTCTTCTGCGTATGCAAAAGCAGATCTTGGT 2302
1743 GAACCTCTGCGCTTCTTCAAGTCTCTCTTCTGCGTATGCAAAAGCAGATCTTGGT 1802
2303 TGCGCAGCTACATGATGAATCTCAACGCGTGGCGCTTGTGTAACAAAAGAGTGC 2362
1803 TGCGCAGCTACATGATGAATCTCAACGCGTGGCGCTTGTGTAACAAAAGAGTGC 1862
2363 TAAGCAATGCCACTTTAGCTG 2383
1863 TAAGCAATGCCACTTTAGCTG 1883

RESULT 3
US-08-620-694A-9
; Sequence 9, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: IL-17 R (hCTLA8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..2693
US-08-620-694A-9

Query Match 3.0%; Score 71.4; DB 2; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;
Qy 1236 ACATGAATGTCGTCAGTGTTCGCCCTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGG 1295
Db 1264 ACGTGGACGTGGTCTGAAATTCGCCAGTTCCTGCTCAGCCTGCGGACGGAAGTGG 1323
Qy 1296 CTCTGGACCTGTGGGAAGACTTTCAGCCTCTGTAGAGAAGGCGAGAGAAATGGGTCTATCC 1355
Db 1324 CCCTGGACCTGTGGAAGAGAGCAGGCCATCTCGGAGGAGGAGTCTGACCTGGGTGGGCC 1383
Qy 1356 AGAAGATCCAGAGTCCAGTTC-----ATCATTTGTGTTTGTTCGAAAGTA 1403
Db 1384 GTCAGAAGCAGGAGATGGTGGAGAGCAACTTAAGATCATCGTCTGTGCTCCCGCGGCA 1443
Qy 1404 TGAAGTACTTTGTGCAAGAAAGAACTACAAACAAAGAGAGGTGGCGCGAGGCTCGGGGA 1463
Db 1444 CGCGCGCAAGTGCAGGCGCTCTTGGGCGGGGGCGCCTGTGGCGGTGGCTCGGACC 1503
Qy 1464 AAGGAGAGCTCTTCTGTGGCGGTGTGAGCAATTCGCGAAAGCTCGCGCAGGCGCAAGC 1523
Db 1504 ACGAAAGCCGCTGGGGAGCCTGTTCACTGAGCATGAAACATGATCTCTCCGGAATTC 1563
Qy 1524 AGATTGCTCGCGCGCTCAGCAAGTTTATCGCGCTTACTTTGATTATTCTTCGCGAGG 1583
Db 1564 AGAGGCCAGCCTGCTTCGGCACTACGTAAGTCTCTTTCAGGAGGTCAAGTGTGAGC 1623
Qy 1584 GAGAGCTCCCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCTC 1643
Db 1624 GCGACGTCCCGCACTGTTTGGCGCGCGCGCGGTACCCGCTCATGACAGGTTCGAGG 1683
Qy 1644 AGCTCTGTTCCTCACTTGCACCTCCGAGACCAAGCGCTTCAGAGCGCGGGGAGCAGCAGC 1703
Db 1684 AGGTGTAATTCGCGCATCCAGGACCTGGAGATGTTCCAGCGCGCGCGCATGACCGCGTAG 1743
Qy 1704 GACAGGGCAGCAGAAAGAACTTCCGAGCAAGTCAAGCGCGTCCCTATATACGTCGCA 1763
Db 1744 GGGAGCTGTTCGGGGGCAACAACCTACCTGCGGAGCGCGGGCGGAGGAGCTCCGCGCGCCC 1803

Qy	1404	TGAAGTACTTTGTGGACAGAGNACTACAAAACAAGAGAGGTGGCCGAGGCTCGGGGA	1463
Db	1444	CGCGCGCAAGTGGCAGCGCTCCTGGGCGGGGGCGCCTGTGCGGCTCGCTGGGACC	1503
Qy	1464	AAGGAGAGCTCTTCCTGGTGGCGGTGTGAGCATTTGCCAAAAAGCTCCGCGCAGGCAAGC	1523
Db	1504	ACGGAAAGCCGGTGGGGGACCTGTTCACTGAGGCCATGAACATGATCTCTCCGGACTTCA	1563
Qy	1524	AGATTCTGTCGCGGGCGCTCAGCAAGTTTATCGCGGTCTACTTTGATTTATTCCTGGAGG	1583
Db	1564	AGAGCCAGGCTGTCTTCGGCACTTACCTAGTCTGCTACTTTCAGCGAGGTGAGTGTGACG	1623
Qy	1584	GAGACGTCGCCGGTATCCTAGACTGAGTACCAAGTACAGACTCATGCAACAACTTCTCCTC	1643
Db	1624	GCGACGTCGCCGACCTGTTTGGCGCGCGCGGTACCGCTCATGGACAGGTTGAGG	1683
Qy	1644	AGTCTCTTTCACCTTGCATCTCCGAGACCAACCGCCTCCAGGAGCGGGGAGCAGCACGC	1703
Db	1684	AGGTGTACTTCCGCACTCCAGACCTGGAGATGTTCCAGCGGGCGCATGCACCGGTAG	1743
Qy	1704	GACAGGCGAGCAGAGAACTACTTCCGGAGCAAGTCAGGCGGTCCCTATAGTCGCCA	1763
Db	1744	GGGAGCTGTTCGGGGGCAACTACTCTGGAGCGCCGGCGGAGGACGCTCCGCGCGCCC	1803
Qy	1764	TTTGCACATGCAACAGTTTATTGACAGGAGCGCGACTGTTTCGAAAAGCAGTTCTGTTTC	1823
Db	1804	TGGACAGTTCGGGACTGGCAGTCCGCTGTCCCGACTGTTTCGATGTGAGAACCTCT	1863
Qy	1824	CCT 1826	
Db	1864	ACT 1866	

RESULT 7

US-09-022-253-9
Sequence 9, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: US98 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93..2693
US-09-022-253-9

Query Match 3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;

QY 1236 ACATGAATGTCGTCCAGTGGTTTCGCCCTACTTCTCCTCAGGACATTCTGTGGCTGTGAGGTGG 1295
DB 1264 ACGTGGACGTGGTCTCTGAANTTCGCCAGTTCCTGTCTCACCGCTCGGCACCAAGAAGTGG 1323
QY 1296 CTCGTGACCTGTGGGAAGACTTCAGCCTCTGTAGAAAGGCGAGAGAAATGGGTCAATCC 1355
DB 1324 CCCTGGACCTGCTGGAAGAGCAGGCCATCTCGGAGCGAGGAGTCATGACCTCGGTGGGGCC 1383
QY 1356 AGAAGATCCACGAGTCCCAGTTC-----ATCATGTGGTTTGTTCTCAAAGGTA 1403
DB 1384 GTCAGAGCAGGAGATGGTGGAGAGCAACTCTAAGATCATCTGTCTCTCCGCGCCA 1443
QY 1404 TGAAGTACTTTGTGGACAAGAAGAACTACAAAACAAAGGAGGTGGCCGAGGCTCGGGGA 1463
DB 1444 CGCGCGCAAGTGGCAGGCGCTCCTGGCCCGGGGGCGCCTGTGCGCTGCGCTGCGACC 1503
QY 1464 AAGGAGAGCTCTTCCTGTGGTGGCGGTGTACGCCATATGCGGAAAAAGCTCGCGCAGGCCAAGC 1523
DB 1504 ACGGAAAGCCGTGGGGGACCTGTTCACTGCAGCCATGAACATGATCTCTCCGAGCTTCA 1563
QY 1524 AGATTCTGTGGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTTGATTATTCCTGGGAGG 1583
DB 1564 AGAGCCAGCGCTGCTTCGGCACCTACGTAGTCTGTACTTTCAGGAGGTGAGCTGTGACG 1623
QY 1584 GAGACGTCCCCGGTATCCTTAGACTGAGTACCAGTACAGACTCATGGACAATCTTCTTCCTC 1643
DB 1624 GCGACGTCCCCGACCTGTTCGGCGCGCGCGCGGTACCCGCTCATGGACAGGTTTCGAGG 1683
QY 1644 AGCTCTGTTCCTCACTTCGCTCAGCAGACCAAGGCTTCAGGAGCGGGGCGAGCACAGC 1703
DB 1684 AGGTGTACTTCCGATCCAGGACCTGGAGATGTTCCAGCCGGGCGCATGACCGCGTAG 1743
QY 1704 GACAGGCGCAGCAAGGAATACTTCCGGAGCAAGTCAGGCGGTCCCTATACGTCCGCCA 1763
DB 1744 GGGAGCTGTGGGGGACACATCTCTGCGAGCCCGGGCGGAGGAGCTCCGCGCGGCC 1803
QY 1764 TTTCGAACATGCAACAGTTTATTGACGAGGAGCCCGACTGGTTTCGAAAAAGCAAGTTCGTT 1823
DB 1804 TGGACAGGTTCCGGGACTGGCAGGTCCGTCTCCCGACTGGTTCGAATGTGAGAACCTCT 1863
QY 1824 CCT 1826
DB 1864 ACT 1866

RESULT 8
US-09-022-260-9
; Sequence 9, Application US/09022260
; Patent No. 6100235

LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93...2693
US-09-022-259-9

Query Match 3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;

QY 1236 ACATGAATGTCTCCAGTGTCTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGG 1295
DB 1264 AGTGGACGTGTCTGAAATTCGCGCAGTCTCTCTCACCCTGCGGCAGGAGTGG 1323

QY 1296 CTCTGGACCTGTGGGAAGACTTTCAGCTCTGTAGAGAGGGCAGAGAAATGGGTATCC 1355
DB 1324 CCTGGACCTGTGGAAGCAGGCGCATCTCGGAGGAGGAGTCTGACCTGGGTGGGCC 1383

QY 1356 AGAAGATCCAGAGTCCCGTTC-----ATCATTTGTGTTTGTTCAGAGGTA 1403
DB 1384 GTCAAGCAGGAGGAGTGTGGAGAGCACTCTTAAGATCATCTGCTGCTCCCGCGCA 1443

QY 1404 TGAAGTACTTTGTGACAGAGAACTACAAACACAAAGAGGTGGCGAGGCTCGGGGA 1463
DB 1444 CGCGGCCAAGTGGCAGGCGCTCTGGGCGGGGGGGCGCTGTGGCTGCGCTCGGACC 1503

QY 1464 AAGGAGAGCTCTTCTGTGTGGCGGTGTACGCCATTCGCGAAAGCTCCGCCAGGCCAAGC 1523
DB 1504 ACGGAAGCCCGTGGGGACCTGTTCACTGACGACCATGAATGATCTCTCCCGACTTCA 1563

QY 1524 AGAGTTGTCGCGGGGCTCAGCAAGTTATCGCGTCTACTTTGATTTCTCTGGAGG 1583
DB 1564 AGAGGCGAGCTGCTTCGGCACCTAGTAGTCTGTCTACTTACGCGAGGTTCAGCTGTGAG 1623

QY 1584 GAGAGCTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGACAACTTCTCTC 1643
DB 1624 GCGAGCTCCCGACCTGTTTCGGCGGCGCGCGGTACCGCTCATGACAGGTTCGAGG 1683

QY 1644 AGCTCTGTTCCCACTTGCACCTCCGAGACACGCGCTCCAGGAGCGCGGCGAGCACGCG 1703
DB 1684 AGGTGTACTTCGCATCCAGGACCTGAGATGTTCCAGCGCGCGCATGACCGGTAG 1743

QY 1704 GACAGGCGAGCAGAGAACTACTTCCGAGCAGAGTTCAGGCGGTCCTTATACGTGCGCA 1763
DB 1744 GGGAGCTGTGGGGGACAACTACTCTCGAGGCGCGGGCGGAGGAGCTCCGCGCGCGCC 1803

QY 1764 TTTGCAATGACCACTTTATGACGAGGCGCGGAGTTCGAAAGCAGTTCGTTTC 1823
DB 1804 TGGACAGGTTCGCGGAGCTGGCAGGTCCCTGTCTCCGAGCTGGTTTCGAATGTGAACTCT 1863

QY 1824 CCT 1826
DB 1864 ACT 1866

RESULT 10
US-09-022-257-9
Sequence 9, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93...2693
US-09-022-257-9

Query Match 3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;

QY 1236 ACATGAATGTCTCCAGTGTCTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGG 1295
DB 1264 AGTGGACGTGTCTGAAATTCGCGCAGTCTCTCTCACCCTGCGGCAGGAGTGG 1323

QY 1296 CTCTGGACCTGTGGGAAGACTTTCAGCTCTGTAGAGAGGGCAGAGAAATGGGTATCC 1355
DB 1324 CCTGGACCTGTGGAAGCAGGCGCATCTCGGAGGAGGAGTCTGACCTGGGTGGGCC 1383

QY 1356 AGAAGATCCAGGTCCTCCAGTTC-----ATCATTTGTGTTTGTTCAGAGGTA 1403
DB 1384 GTCAGAGCAGGAGAGTGTGGAGAGCACTCTTAAGATCATCTCTCTCTCCCGCGCA 1443

QY 1404 TGAAGTACTTTGTGACAGAGAACTACAAACACAAAGAGGAGTGGCGGAGGCTCGGGGA 1463
DB 1444 CGCGGCCAAGTGGCAGGCGCTCTCTGGGCGGGGGCGCTCTGCGGCTGCGCTGCGACC 1503

QY 1464 AAGGAGAGCTCTTCTGTGGCGGTGTGAGCCATTCAGCCATTCGCCGAAAGCTCCGCCAGGCCAAGC 1523
DB 1504 ACGGAAGCCCGTGGGGACCTGTTCACTGACGACCATGAATGATCTCTCCCGACTTCA 1563


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/ Sequence 1, Application US/09022255
/ Patent No. 6072033
/ GENERAL INFORMATION:
/ APPLICANT: Yao, Zhengbin
/ APPLICANT: Spriggs, Melanie
/ APPLICANT: Fanslow, William
/ TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Immunex Corporation
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Power Macintosh
/ OPERATING SYSTEM: Apple Operating System 7.5.5
/ SOFTWARE: Microsoft Word for Apple, Version 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/022,255
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/620,694
/ FILING DATE: 21 MARCH 1996
/ APPLICATION NUMBER: USSN 08/538,765
/ FILING DATE: 7 AUGUST 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/410,535
/ FILING DATE: 23 MARCH 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,695
/ REFERENCE/DOCKET NUMBER: 2617-B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3288 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Mouse
/ STRAIN: HVS13 receptor
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 121..2715
/ US-08-620-694A-1

Query Match 2.3%; Score 54.6; DB 2; Length 3288;
Best Local Similarity 48.0%; Pred. No. 0.00011;
Matches 156; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 1503 AAAAGCTCGCGCAGCAAGCAGAGTTCGTCCGCGCGCTCAGCAAGTTTATCGCGTCT 1562
DB 1580 ACATGATCTCGCAGACTTCAAGAGCGCAGCTGCTTCGGCACCTACGTTGTTGCTACT 1639
QY 1563 ACTTTGATTATTCCTGCGAGGAGACGTCCTCCCGGTATCTAGACCTGAGTACCAAGTACA 1622
DB 1640 TCAGTGGCATCTGTAGTGAGAGGGATGTCCTCCGACCTCTTCAACATCACCTCCAGGTACC 1699
QY 1623 GACTCATGACAACTCTTCTCCTGAGTCTGTTCCACTTCCGAGACCGGCTCC 1682
DB 1700 CACTCATGACAGATTGAGGAGGTTTACTTCCGATCCAGACCTGGAGATGTTTGAAC 1759
QY 1683 AGGAGCCGGGCGAGCAGCAGCGAGGAGGAGGAACTACTTCCGGAGCAAGTACAG 1742
DB 1760 CCGGCGGATGACCATGTGACAGAGCTCACAGGGAGCAATTTACCTGCAGAGCCCTAGTG 1819
QY 1743 GCGGTCCTATACGTGCGCATTTGCAATGACAGTTTATTGACGAGGAGCCGACT 1802
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DB 1880 GGTTCGAGCGTGAGAACCTCTGCTT 1904

RESULT 13
US-09-022-255-1
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RESULT 14

US-09-022-696-1
; Sequence 1, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
US-09-022-696-1

Query Match 2.3%; Score 54.6; DB 3; Length 3288;
Best Local Similarity 48.0%; Pred. No. 0.00011;
Matches 156; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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RESULT 15

US-08-978-773-1
; Sequence 1, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Trout, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2623-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; IMMEDIATE SOURCE:

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GenCore version 5.1.6
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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3: gb_hic.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	1033.8	43.4	1674	AY408491	AY408491 Mus muscu
4	578.8	24.3	583	BP275741	BP275741 BP275741
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ALIGNMENTS

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DEFINITION Homo sapiens HCM3241 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY408489
VERSION AY408489.1 GI:39764460
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1677)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1677)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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LOCUS
DEFINITION Pan troglodytes HCM3241 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY408490
VERSION AY408490.1 GI:3976461
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 1677)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1677)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-Nov-2003) Celera Genomics, 45 West Gude Drive,
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Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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ORIGIN
 Query Match 63.6%; Score 1515.8; DB 9; Length 1677;
 Best Local Similarity 92.5%; Pred. No. 0;
 Matches 1654; Conservative 0; Mismatches 23; Indels 111; Gaps 2;
QY 560 ATGGAATCTCAACCTTCTGTAATGAAATTTGAAACGGATATTTTGGTAAAGTTGTC 619
DB 1 ATGGAATCTCAACCTTCTGTAATGAAATTTGAAACGGATATTTTGGTAAAGTTGTC 60
QY 620 CTTTTTCTTCCATTAAACGAAAGCAATTAACACCTTTCTTTTAGAACCCGAGCC 679
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RESULT 3

AY408491

LOCUS

DEFINITION

Mus musculus HCM3241 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION

AY408491.1

VERSION

AY408491.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1674)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarilal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1674)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarilal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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source Location/Qualifiers
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Qy 230 CCCCGGCTTTGTGTTGCTAAATGAGGAGTGGGGGCGGACGACAGAAACAGTGGCTGTAC 289
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Db 620 GCTTGTAACCCCTTCTGGAAGCTCGGAACCTGGAACATCAGCAGCATGGCTCGGACATG 679
Qy 770 CAGGTGTCCTTCGACCATGACCGCACAACTTCGGCTTCGTTTC 814
Db 680 CANGTGTCTTCGACCATGACCGCACAACTTCGGCTTCGTTTC 724

RESULT 6
CV126214
LOCUS
DEFINITION
IMAGE:7453313 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 748)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Plate: LLAM15711 row: p column: 15
High quality sequence stop: 689.

FEATURES
source
Location/Qualifiers
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Note: Organ: testis; Vector: pExpress-1; Site 1: EcoRV;
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animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTAGTTCATGATCGAGCGGCCGCCCTT-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 1.9 kb. This primary
library is normalized (non-normalized primary library is
NIH_MGC 237) and was constructed by Express Genomics
(Frederick, MD)"

ORIGIN

Query Match 19.7%; Score 469.4; DB 7; Length 748;
Best Local Similarity 78.3%; Pred. No. 1.4e-119;
Matches 589; Conservative 0; Mismatches 154; Indels 9; Gaps 2;

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Db 181 CCATTGCTGAGAGCTCCGTCAAGCCAGCAGAGAGCTCATCTCGCGGCACTGAGCAAGTTCA 240

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Db 595 GGCCAGAAAGTGAATCTCTGCTTAAGTATGAGAGCTTCTATCTTGGGGCACTGGGCCAG 654

Qy 1974 CCGACTCCAGCAGAGAGTCAAGTGGGGGCTGGACCAAGAGCGGGAGGCCCGGCCTG 2033

303 CCTATACGTCGCCATTGCAACATGCAACAGTTTATTGACGAGGAGCCGACTGGTTCG 362
 1809 AAAAGCAGTTTCGTTCCCTTCCATCTCTCCACTCGCGCTACCGGAGCCAGTCTTTGAGA 1868
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 1869 AATTTCGATTCGGGCTTGGTTTAAATGATGTCATGTGCAA 1908
 423 AATTTCGATTCGGGCTTGGTTTAAATGATGTCATGTGCAA 462

BB616055 649 bp mRNA linear EST 26-OCT-2001
 BB616055 RIKEN full-length enriched, adult male testis Mus musculus
 cDNA clone 4931403M23 5', mRNA sequence.
 BB616055
 BB616055.1 GI:16456248
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 649)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanaoka, T.,
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
 Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, P.,
 Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.,
 and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11) 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.
 Location/Qualifiers
 1. .649
 /organism="Mus musculus"
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FEATURES
 source

transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1."

ORIGIN

Query Match 18.2%; Score 433; DB 2; Length 665;
Best Local Similarity 83.6%; Pred. No. 2.2e-109;
Matches 521; Conservative 0; Mismatches 60; Indels 42; Gaps 1;
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QY 655 CCCTTTCTTTCTTAGAACCCGAG 677
DB 560 TCCCTTCTTCTTCAGAACCGGG 582

RESULT 10

LOCUS BE750478 547 bp mRNA linear EST 25-APR-2001
DEFINITION 201867 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE750478
VERSION BE750478.1 GI:10164470
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 547)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberte,A.J., Stone,R.T.,

Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A.,
Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Smith TPL
11282978
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCAAGCAGC
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FEATURES

source

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Library made from pooled tissue from day 20 and day 40
embryos."

ORIGIN

Query Match 18.1%; Score 431; DB 2; Length 547;
Best Local Similarity 86.1%; Pred. No. 7.4e-109;
Matches 507; Conservative 0; Mismatches 40; Indels 42; Gaps 1;
QY 70 GGGCGAGCGCAGCGCCATGGCCCGTGGCTGCGAGCTCTGCTCCGCTCTTTACGGTCAA 129
DB 1 GGGCGAGCGCAGCGCCATGGCCCGTGGCTGCGAGCTCTGCTCCGCTCTTTACGGTCAA 60
QY 130 CGCTGCTCTCAACGGCTCGCAGCTGGCTGTGGCCGCTCGCGGCTCGCGCGCGGG 189
DB 61 CGCTGCTCTCAACGGCTCGCAGCTGGCTGTGGCTCGCGGCTCGCGAGCGCGGG 120
QY 190 CGCCGACACCTGTGGCTGGAGATGAAGCGGCTGCCCGACCCCGCTTTGTGTGCTAA 249
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QY 430 GGGCCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTAATCTACTGGAGGAGCTCAAGTCGA 489
DB 319 GGGCCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTCATCTGAGGAGCTGAAGTCAGA 378
QY 490 GGGAGACAGTGCACCACTGATTTCTAAAGGATCCGAGCAGCTCAACAGTAGCTTCAA 549
DB 379 GGGAGCAGAGTGCACCACTGATTTCTAAAGGACCCGAGCAGCTCAACAGTAGCTTCAA 438
QY 550 AAGAAGTGAATGGAATCTCAACCTTTCTCTGAATATGAATTTTGAACGGATTTATTTCTGT 609

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439 AAGAGCTGGGATGGAATCTCAACCTTCTCGAATGAAATTTGAACAGATTACTTGT 498
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610 AAAGTTGTCCTCTTTCTCCATTAATAAAGCAAGCAATTACCACTT 658
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499 AAGATCGCTCTTCTCTCCATTAATAAAGCAAGCAATTATCACCT 547
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RESULT 11
BU221978 692 bp mRNA linear EST 25-NOV-2002
LOCUS 603105617F1 CSEQCHN04 Gallus gallus cdna clone CHEST44a6 5', mRNA
DEFINITION
ACCESSION BU221978.1 GI:25410688
VERSION BU221978
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 692)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1...692
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/db_xref="taxon:9031"
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/clone_lib="CSEQCHN04"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo (dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

Query Match 17.8%; Score 424.4; DB 5; Length 692;
Best Local Similarity 76.4%; Pred. No. 5.7e-107;
Matches 521; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 417 TTTGGTCCCGAGGGCCCTCGCATCGAATTCCTGAAGGATTCGGGTAACTACGGAGG 476
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DB 11 TTTGACAGCAAAATGCCATTGGATTGAATACCTGAGAGGATTCGCGTAACTATTGAAG 70
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QY 477 AGCTGAAGTCGGAGGGAAGACAGTCCCAACAACTGATTCCTAAAGGATCCGGAAGCAGCTCA 536
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Db 71 AGTTAAATCAGAGGGGAAGCAATGTGTCAGCAGATGGTTTTTAAGAGATCCAAAGCAGCTCA 130
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DB 131 GCCCAAGTTTTAAAGAAACAGGAATGGAATCCATCCCTTTTGCAAAATCTGAAGTTTGAAA 190
QY 597 CGGATTATTTTCGTAAGGTTGTCCCTTTTCCATTAAATAAAGCAAGCAATTTACCACC 656
DB 191 CAGATTACTTTGTCAAGATTGTGCTTTTCTTCCATTAATAAAGTAAATATATCACC 250
QY 657 CTTTCTTTTAGAACCAGGCTGTGACCTGTGTTTACAGCCGGAACAATCTAGCTGTGA 716
DB 251 CATTCTTTTCCGAACTCGGCCATGTGAATTAATTGCTACAGCCAGAAAAACCTCATCTGCA 310
QY 717 AACCTTTCTGGAAGCCTCGGAACCTGAACATCAGCAGCATGGCTCGGACATGCAGGTGT 776
DB 311 AACCTTACTGGAAGCCACGGAATCTGAATGTTACCCAGCAGGGTTTAAATATGCAAGTGT 370
QY 777 CTTTCGACCATGCAACCGCAACAATTTCCGCTTCCGTTTCTTCTATCTTCACTTACAAGTCA 836
DB 371 CTTTGTGATCATGCTCCCAACAACCTTTCGATTTAGATATTACTTTCTTCACTACAACTGA 430
QY 837 AGCAAGAAAGCACTTTTCAAGCGAAAGACCTGTAAAGCAGGAGCAAACTACAGAGACGACCA 896
DB 431 AGCATGAAGGGCCATTCAAGCAAAAGACCTGCAAAACAGGATCAAAAACACAGATACTACAA 490
QY 897 GCTGCTCTCTTCAAAATGTTTCTCCAGGGATTAATAATTGAGCTGCTGGATGACACTA 956
DB 491 GTTGTATTCTTCAGAATGTAACTCCAGGGATTAATAATCATCGAGCTGGTGATGACACTA 550
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QY 1017 CCATCAGAGCGGTGGCCATCAGTGCACATGCTGGTAGTCAATATCGGAGATTCGCGACGCTCT 1076
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QY 1077 TCATGTGATGTGCGCGCAAGAA 1098
DB 671 TCACAGTGTGTCGCGCAAAAA 692

RESULT 12
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LOCUS 603843254F1 CSEQREN22 Gallus gallus cdna clone CHEST828k13 5', mRNA
DEFINITION
ACCESSION BU479802
VERSION BU479802.1 GI:25973379
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 717)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1...717

FEATURES
source
BU479802
LOCUS 603843254F1 CSEQREN22 Gallus gallus cdna clone CHEST828k13 5', mRNA
DEFINITION
ACCESSION BU479802
VERSION BU479802.1 GI:25973379
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 717)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1...717

FEATURES
source
```


RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
SOURCE

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1. 667
location, qualifications
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/tissue_type="egg"
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/lab_note="DH108"
/clone lib="RIKEN full-length enriched, 2 cells egg"
/notes="Site 1: Sall; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTTTNN 3', cDNA was
prepared by using trihalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by the
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence 15'
GAGAGAGAGATCTCCAGTAAATTAATATATCCCCCCCCCCCC 3'. cDNA
was cleaved with XhoI and BamHI. Vector: a modified
pBluescript KS(-) after bulk excision from Lambda FLC I."

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ORIGIN

Query Match	17.5%;	Score 416;	DB 6;	Length 667;
Best Local Similarity	87.8%;	Pred. No. 1.3e-104;		
Matches 452;	Conservative 0;	Mismatches 63;	Indels 0;	Gaps 0;
QY	252	AGGAGTGGGGCCAGCCAGCAGAGAAACAGTGGGCTGTACAAACATCACCTTCAAAATATGACA	311	
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QY	312	ATTGTACCACTTCTTGAATCCAGTGGGGAAGCATGTGATTTGTGACGCCCGCAGAAATATCA	371	
DB	213	ACTGTACCACTTCTTGAATCCCGCGGGAAGCATGCGATTGTGTGATGCTCAGAAATATCA	272	
QY	372	CCATCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCCACATTTCTTTGGTCCCCAGGGG	431	
DB	273	CCATCAGCCAGTACGCTTTGCCACGGCAGAGTGGCAGTCCACATTTCTTTGGTCCCCAGGGG	332	
QY	432	CCCTCGGCATCGAATTCCTGAAAGGATTTCCGGTAAATCTGGAGGAGCTGAAAGTCGAGG	491	
DB	333	CCCTTGGCAITGAATTCCTAAAAGGATTCGAGTTCATCCTGGAGGAGCTGAAAGTCGAGG	392	
QY	492	GAAGACAGTGGCCACCAACTGATTTCTAAGGATCCGAAGCAGCTCAACAGTAGCTTTCAAAA	551	
DB	393	GCAGACAGTGGCCAAACAGTGATTTCTAAGGAGCCCAACAGCTCAACAGCAGCTTTAGAA	452	
QY	552	GAACTGGAATGGAACTCTCAACCTTTCCTGAAATATGAAATTTGAAACGGATTTATTTCTGTA	611	
DB	453	GGACTGGAATGGAACTCTCAGCTTTCCTGAAATATGAAATTTGAGACGGATTTACTTTGTAA	512	
QY	612	AGGTTGTCCTTTTTCCTTCCATTTAAAAACGAAAGCAATTAACCCCTTTCTTCTTTAGAA	671	
DB	513	AGATTGTCCTTTTTCCTTCCATTTAAAAATGAAGCAATTAACATCCCTTTCTTCTTCGAA	572	
QY	672	CCCGAGCCTGTGACCTGTGTTGTTACAGCGGAGCAATCTAGCTTTGTAAAAACCCCTTCTGGGAGC	731	

Db 573 CACGGGCTGTGACCTGTTTGTAACTGANCACCTTGGCCTGNTACCTTTCCTGAAGC 632

Qy 732 CTGGGAACCTGAACATCAGCCAGCATGGCTCGGAC 766

Db 633 CTGGAACCTTGAATATCAGCCAGCATGGTTCTGAC 667

RESULT 14

BQ830554	548 bp	linear	EST 15-SEP-2002
LOCUS			
DEFINITION	L61in20509 AFT024-subtracted library Mus musculus cDNA 5' similar to Hypothetical human protein DKF2p434N1928, mRNA sequence.		
ACCESSION	BQ830554		
VERSION	BQ830554.1		
KEYWORDS	GI:22862622		
SOURCE	EST.		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 548)		
AUTHORS	Hackney,J.A., Charbord,P., Brunk,B.P., Stoeckert,C.J., Lemischka,I.R. and Moore,K.A.		
TITLE	A molecular profile of a hematopoietic stem cell niche		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066 (2002)		
MEDLINE	22247628		
PUBMED	12226475		
COMMENT	Contact: Moore, Kateri A.		

FEATURES

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1. .548
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/db_xref="taxon:10090"
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/lab_host="DH10B"
/clone_lib="AFT024-subtracted library"
/note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site 2: Not 1; Two directionally cloned cDNA libraries were made from a hematopoietic stem cell-supporting stromal cell line (AFT024) and from a non-supporting stromal cell line (2018). Subtractive hybridization was performed by hybridization of the target, AFT024, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, 2018 cDNA library in pSport2 with inserts cloned in the complementary orientation. The AFT024-subtracted library contains 4.2x105 clones and is depleted of common housekeeping gene products eg. beta-actin and enriched for transcripts specific to AFT024. For detailed protocols and additional information please see our website at http://stromalcell.princeton.edu."

```

ORIGIN

Query Match 17.4%; Score 414.4; DB 5; Length 548;
Best Local Similarity 85.1%; Pred. No. 3.3e-104;
Matches 463; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
Qy 527 AAGCAGCTCAACAGTACGTTCAAAGAACGTGGAAATCTCAACCTTTCCTGAATG 586

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 03:35:56 ; Search time 1906 Seconds

(without alignments)
3787.947 Million cell updates/sec

Title: US-10-717-282-1_COPY_86_234

Perfect score: 149

Sequence: 1 atggcccgctggctgcagct.....aaagcggtgccgaccocg 149

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	100.0	2383	6	AX364570 Sequence
2	149	100.0	2383	6	AX364573 Sequence
3	127	85.2	2341	6	AX364576 Sequence
4	127	85.2	2724	9	AF458067 Homo sapi
5	127	85.2	4392	6	AX392973 Sequence
6	127	85.2	4477	9	AF494208 Homo sapi
7	126.8	85.1	154606	9	AC097358 Homo sapi
8	125.4	84.2	2037	9	AB093642 Macaca fa
9	123.8	83.1	3083	6	AX351723 Sequence
10	122.4	82.1	2786	6	AX350979 Sequence
11	112.6	75.6	2203	10	BC066804 Mus muscu
12	112.6	75.6	2387	10	AF494210 Mus muscu
13	112.6	75.6	2443	6	AX364580 Sequence
14	112.6	75.6	3366	10	AF459444 Mus muscu
15	112.4	75.4	134122	10	AC125152 Mus muscu
16	112.4	75.4	179891	2	AC116282 Rattus no
17	110.8	74.4	258797	2	AC116282 Rattus no
18	110.8	74.4	295304	2	AC119550 Rattus no
19	104.6	70.2	2259	6	AX364572 Sequence

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21	88.8	59.6	2217	6	AX364578	AX364578 Sequence
22	87.8	58.9	2217	6	AX364582	AX364582 Sequence
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c	37	38	25.5	2262	6	CO716916 Sequence
c	38	38	25.5	2320	9	BC022016 BC022016 Homo sapi
c	39	38	25.5	2547	8	AY328910 AY328910 Oryza sat
c	40	38	25.5	4498	8	AY328909 AY328909 Oryza sat
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c	42	38	25.5	144189	9	AC023891 AC023891 Homo sapi
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ALIGNMENTS

RESULT 1	AX364570	Sequence 1 from Patent WO208259.	2383 bp	DNA	linear	PAT 15-FEB-2002
LOCUS	AX364570					
DEFINITION	AX364570					
ACCESSION	AX364570.1	GI:18696530				
VERSION	AX364570.1	GI:18696530				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1					
AUTHORS	Presnell,S.R., Kuestner,R.E. and Gao,Z.					
TITLE	Human cytokine receptor					
JOURNAL	Patent: WO 0208259-A 1 31-JAN-2002;					
FEATURES	ZymoGenetics, Inc. (US)					
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	VSPGVITIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVIISAFATLFTVM					
	CFKQKQENTYSHLDRESSSTYTAALPRRLRPKPVLCYSSKQGMNVVQCFPA					
	YFLQFCGCEGLDLWEDESLSLCREQREWVQIKIHESQFIIVCSKGMKVFVDKNKY					
	HKGFGSGSGELFLVAISAIKLRQAQSSAALSFKIAIVFYDSCGSDVPGILDIL					
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CDS

ORIGIN

AUTHORS	Gilbert, J.M. and Gorman, D.M.
TITLE	Identification of novel IL-17 related receptors
JOURNAL	Unpublished
REFERENCE	2. (bases 1 to 2724)
AUTHORS	Gilbert, J.M. and Gorman, D.M.
TITLE	Direct Submission
JOURNAL	Submitted (13-DEC-2001) Genomics, DNAX Research Inc., 901 California Ave., Palo Alto, CA 94304, USA
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ORIGIN

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Query Match      85.2%; Score 127; DB 9; Length 4477;
Best Local Similarity 93.0%; Pred. No. 5.7e-16;
Matches 133; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 90 ATGGCCCCGTGCTGACGCTGCTCCTCTTTTACGGTCAACGCTGCTCAACGGC 149

QY 61 TCGCAGCTGGCTGGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 150 TCGCAGCTGGCTGGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 209

QY 121 TGGAGGATGAAGCGCTGCTCCCG 143
Db 210 TGGAGGGAGTGGGGCAGCCAG 232
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RESULT 7
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DEFINITION Homo sapiens chromosome 3 clone RP11-157F20, complete sequence.
ACCESSION AC097358
VERSION AC097358.2 GI:21166205
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154606)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
Haugen, E.D.
Direct Submission
Unpublished
2 (bases 1 to 154606)
Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.
Direct Submission
Submitted (16-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 154606)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
Haugen, E.D.
Direct Submission
Submitted (24-MAY-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On May 24, 2002 this sequence version replaced gi:16152308.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
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Web site: http://www.genome.washington.edu
Contact: uwchgsgs@u.washington.edu
Project Information
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Center project name: chr-3
Center clone name: RP11-157F20 (bc0274)
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----- Summary Statistics
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET; 96% of reads
Chemistry: Dye-terminator Big Dye; 4% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154096 bases at least Q40
Consensus quality: 154548 bases at least Q30
Consensus quality: 154600 bases at least Q20
Insert size: 154606; sum-of-contigs
Quality coverage: 8.5x in Q20 bases; sum-of-contigs
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Overlapping Sequences:

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5': RP11-263116 (UWGC:bc0327) AC092050, 123826-bp overlap
3': RP11-241K3 (UWGC:bc0319) AC093928
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Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII			EcoRI			BglII		
SeqDerMap	FngerPrint	SeqDerMap	FngerPrint	SeqDerMap	FngerPrint	SeqDerMap	FngerPrint	
3231	3121	8696	8585	3265	3145			
6382	6538	6	<800	2067	2073			
512	<800	7382	7337	6892	7026			
449	<800	4493	4449	16	<800			
14536	14523	4776	4809	679	<800			
2492	2542	10400	10102	5157	5118			
710	<800	635	<800	695	<800			
1773	1776	6842	6855	4557	4598			
1817	1776	30273	30419	172	<800			

Matches	129;	Conservative	0;	Mismatches	14;	Indels	0;	Gaps	0;
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b	70	ATGGCCCCGCTGCAGCTCTGCTCCGCTCTTTACGGTCAACGGCTGCCTCAACGGC	129						
y	61	TCGCAGCTGGCTGTGGCCGCTGGGGGGTTCGGCCGCGCGGGGGCGCGACCTCTGTGC	120						
b	130	TCGCAGCTGGCTGTGGCCGCTGGGGGGTTCGGCCGCGCGGGGGCGCGACCTCTGTGC	189						
y	121	TGGAGGATGAACGGCTGCCCG	143						
	190	TGGANGGGAGTGGGCCAGCCAG	212						

RESULT 11					
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OCUS	BC066804				
DEFINITION	BC066804				
ACCESSION	BC066804.1				
VERSION	BC066804.1				
					GI:45219858
					ROD 05-MAR-2004

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2203)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D.,
Altchul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903	(2002)
PUBMED	12477932				
REFERENCE	2	(bases 1 to 2203)			
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapps-remail.nih.gov
Tissue Procurement: Dr. Angelo L. Vescovi (Institute fro Stem Cell
Research, Italy)
cDNA Library Preparation: Yulan Piao and Minoru Ko (National
Institute on Aging, NIH: <http://agsun.grc.nia.nih.gov/cDNA/>)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-sbgs.stanford.edu>
Contact: (Dickson, Mark) mcdopaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 24025661.

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RESULT 12
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ORIGIN

Query Match 75.6%; Score 112.6; DB 10; Length 2387;
Best Local Similarity 86.7%; Pred. No. 4.7e-13;
Matches 124; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy 121 TGGAGGATGAAGCGGCTGCCCG 143
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RESULT 13
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DEFINITION Sequence 11 from Patent WO0208259.
ACCESSION AX364580
VERSION AX364580.1 GI:18696539
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Preenell, S.R., Kuestner, R.E. and Gao, Z.
Human cytokine receptor
Patent: WO 0208259-A 11 31-JAN-2002;
ZymoGenetics, Inc. (US)

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Query Match 75.6%; Score 112.6; DB 6; Length 2443;
Best Local Similarity 86.7%; Pred. No. 4.7e-13;
Matches 124; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy 61 TCGCAGCTGGCTGTGGCGCGTGGCGGGTCCGGCGCGCGCGCGACACCTGTGGC 120
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Qy 121 TGGAGGATGAAGCGGCTGCCCG 143
Db 221 TGGAGGAGTGGGGCGGCCAG 243

RESULT 14
AF459444

LOCUS AF459444 3366 bp mRNA linear ROD 15-MAY-2002
DEFINITION Mus musculus transmembrane protein (Sef) mRNA, complete cds.
ACCESSION AF459444
VERSION AF459444.1 GI:20799327
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Lin, W., Furthauer, M., Thisse, B., Thisse, C., Jing, N. and Ang, S.L.
Cloning of the mouse Sef gene and comparative analysis of its
expression with Fgf8 and Spry2 during embryogenesis
Mech. Dev. 113 (2), 163-168 (2002)
21959295
11960706
REFERENCE 2 (bases 1 to 3366)
AUTHORS Lin, W. and Ang, S.-L.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2001) I.G.B.M.C., 1, rue Laurent Fries, Iilkirch
67404, France
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Best Local Similarity 91.5%; Pred. No. 2.8e-13;
Matches 119; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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Qy 61 TCGCAGCTGGCTGTGGCCGCTGGCGGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
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Qy 121 TGGAGGATGA 130
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Search completed: August 16, 2005, 04:28:47
Job time : 1913 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 03:30:47 ; Search time 432 Seconds
(without alignments)
2041.763 Million cell updates/sec

Title: US-10-717-282-1_COPY_86_234

Perfect score: 149

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 9: geneseqn2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	149	100.0	2383	6	ABA95031 Human cyt
2	149	100.0	2383	6	ABA95033 Human cyt
3	127	85.2	2341	6	ABA95035 Human cyt
4	127	85.2	4392	6	ABK62082 Human cdn
5	123.8	83.1	3083	4	AAS15346 DNA encod
6	122.4	82.1	2786	6	AAS18134 Human DNA
7	112.6	75.6	2443	6	ABA95037 Murine cy
8	104.6	70.2	2259	6	ABA95034 Human cyt
9	104.6	70.2	2259	6	ABA95032 Human cyt
10	88.8	59.6	2217	6	ABA95036 Human Zcy
11	87.8	58.9	2217	6	ABA95038 Murine cy
12	83.6	56.1	2214	6	AAS18135 Human DCR
13	81.6	27.9	18876	10	ADI23928 Streptomy
14	41.6	27.9	61944	8	ADI23920 Streptomy
15	38.4	25.8	567	8	ACA26238 Prokaryot
16	38	25.5	1407	12	ADM94405 Rice brit
17	38	25.5	2196	2	AAQ71197 Human pro
18	38	25.5	2196	3	AAA35296 Human ade
19	38	25.5	2196	3	AAF21418 Human low
20	38	25.5	2196	10	ABZ97112 Human nuc

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c	22	38	25.5	2196	12	ADI81649	Adi81649 Human pro
c	23	38	25.5	38644	3	AAA35302	Aaa35302 Human ade
c	24	38	25.5	38644	3	AAF21424	Aaf21424 Human low
c	25	38	25.5	38644	10	ABZ97118	Abz97118 Human nuc
c	26	38	25.5	38644	11	ABD20967	Abd20967 Human pul
c	27	38	25.5	80928	12	ADO25290	Ado25290 Human pro
c	28	36	24.2	1671	4	ABL09901	Abi09901 Drosophil
c	29	36	24.2	1671	4	ABL09900	Abi09900 Drosophil
c	30	35.6	23.9	1620	4	AAS51502	Aas51502 Pseudomon
c	31	35.6	23.9	1620	8	ACA19515	ACA19515 Prokaryot
c	32	35.6	23.9	1674	11	ABD03041	Abd03041 Pseudomon
c	33	35.6	23.9	1785	11	ABD02924	Abd02924 Pseudomon
c	34	35.2	23.6	2757	8	ACA25644	ACA25644 Prokaryot
c	35	35.2	23.6	4010	4	AAS11603	Aaa11603 Chicken c
c	36	34.8	23.4	17955	2	AAV56642	Aav56642 Actinopla
c	37	34.6	23.2	474	9	ACH14819	Ach14819 Human adu
c	38	34.6	23.2	1367	4	AAD16506	Aad16506 Human ABC
c	39	34.6	23.2	1367	5	AAS29733	Aas29733 Human end
c	40	34.6	23.2	1367	9	ADA27261	Ada27261 cDNA enco
c	41	34.6	23.2	1367	10	ADA12864	Ada12864 Human ABC
c	42	34.6	23.2	1437	5	AAS29631	Aas29631 Human end
c	43	34.6	23.2	2383	4	AAH18672	Aah18672 Human cDN
c	44	34.6	23.2	2392	11	ADM01573	Adm01573 Human cDN
c	45	34.6	23.2	2487	4	AAH14983	Aah14983 Human cDN

ALIGNMENTS

RESULT 1

ABA95031

ID ABA95031 standard; DNA; 2383 BP.

AC ABA95031;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 nucleotide sequence.

KW Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 86..2347

FT /*tag= a

FT /product= "Zcytor18"

PN WO2002082559-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX P-PSDB; ABB07626.

XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.

XX Claim 5; Page 85-90; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide

CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 nucleotide sequence

SQ Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 U; 0 Other;
Query Match 100.0%; Score 149; DB 6; Length 2383;
Best Local Similarity 100.0%; Pred. No. 1e-26;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGGCTGCTCAACGGC 60
Db 86 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGGCTGCTCAACGGC 145
QY 61 TCGAGCTGGCTGTGGCCGCTGGCGGTCCTGGCCGCGCGCGGGCGCGACACCTGTGGC 120
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QY 121 TGGAGGATGAAGCGGCTGCCCGACCCCG 149
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RESULT 2
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ID ABA95033 standard; DNA; 2383 BP.
AC ABA95033;
XX
DT 20-MAY-2002 (first entry)
XX
DE Human cytokine receptor, Zcytor18 variant nucleotide sequence.
XX
KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 86..2347
FT FT /*tag= a
FT FT /product= "Zcytor18 variant"
XX
PN WO200208259-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023253.
XX
PR 26-JUL-2000; 2000US-0220747P.
XX
PR (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kuestner RE, Gao Z;
XX
DR WPI; 2002-217048/27.
DR P-PSDB; ABB07627.
XX
PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.

PS Disclosure; Page 94-98; 119pp; English.
XX
CC The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 variant nucleotide sequence

SQ Sequence 2383 BP; 558 A; 681 C; 638 G; 506 T; 0 U; 0 Other;
Query Match 100.0%; Score 149; DB 6; Length 2383;
Best Local Similarity 100.0%; Pred. No. 1e-26;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGGCTGCTCAACGGC 60
Db 86 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGGCTGCTCAACGGC 145
QY 61 TCGAGCTGGCTGTGGCCGCTGGCGGTCCTGGCCGCGCGGGCGCGACACCTGTGGC 120
Db 146 TCGAGCTGGCTGTGGCCGCTGGCGGTCCTGGCCGCGCGGGCGCGACACCTGTGGC 205
QY 121 TGGAGGATGAAGCGGCTGCCCGACCCCG 149
Db 206 TGGAGGATGAAGCGGCTGCCCGACCCCG 234

RESULT 3
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ID ABA95035 standard; DNA; 2341 BP.
AC ABA95035;
XX
DT 20-MAY-2002 (first entry)
XX
DE Human cytokine receptor, Zcytor18 splice variant nucleotide sequence.
XX
KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 86..2305
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FT FT /product= "Zcytor18 splice variant"
XX
PN WO200208259-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023253.
XX
PR 26-JUL-2000; 2000US-0220747P.
XX
PR (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kuestner RE, Gao Z;
XX
DR WPI; 2002-217048/27.
DR P-PSDB; ABB07628.
XX
PT New cytokine receptor polypeptide designated zcytor18, useful for

Qy 121 TGGAGGATGAAAGCGGCTGCCCG 143
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 Db 190 TGGANGGGAGTGGGGCCAGCCAG 212

RESULT 7
ABA955037
ID ABA955037 standard; DNA: 2443 BP.

ABA95037;
20-MAY-2002 (first entry)

DE Murine cytokine receptor, Zcytor18 nucleotide sequence.

Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW
pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW
erythroleukemia; chromosome 3p14.3; gene therapy; mouse; ds.
KW

SO
MUG 8p.

	Key	Location/Qualifiers
CDS		101..2320
FT		/tag= a
PT		/product= "mouse ZC

PN WO200208259-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US023253.

26-JUL-2000: 2000US-0220747P.

AA (ZYMO) ZYMOGENETICS INC. PA

PI Presnell SR, Kuestner RE, Gao Z;

WPI; 2002-217048/27.
P-PSDB: ABB07630.

New cytokine receptor polypeptide designated zcvtor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcvtor18 ligand.

XX
PS
Claim 7: Page 111-115: 119pp: English.

The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 *in vivo* by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for *in vivo* diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a murine Zcytor18 nucleotide sequence.

Sequence 2443 BP; 564 A; 700 C; 642 G; 537 T; 0 U; 0 Other;

Query Match 75.6%; Score 112.6; DB 6; Length 2443;
Best Local Similarity 86.7%; Pred. No. 6.1e-18;
Matches 124; Conservative 0; Mismatches 19; Indels 0;

Qy 1 ATGGCCCCGTGGCTGAGCTCTGCTCCGTCTTCTTTACGGTCAACGGCTGCTCAACGGC 60

Dh 101 ATGGCCCCGGGCGGAGCTGCTGCTCTTCTTCACTGTCAACGGCTGTCTCAACGGC 160

61 TCGAGCTGGCTGTGGCCGGCTGGCCGGTCCGGCCGGCGGGCGCCGACACCTGTGGC 120

Db 161 TCGCAGCTGGCAGTGGCGCGCGCGCGGTCCGCGCCGCGCAGGGGCGCGGACCTGTGGC 220

Qy 121 TGGAGGATGAAGCGGCTGCCCCG 143

Db 221 TGGAGGGGAGTGGGGCGGGCCAG 243

RESULT 8

ABA95034

ID ABA95034 standard; DNA; 2259 BP.

AC ABA95034;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 variant degenerate coding sequence.

Cytokine receptor; Zcytor18; cell proliferation; antiprosoriatic; human;
KW
pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW
erythroleukemia; chromosome 3p14.3; gene therapy; ds.
KW

OS Homo sapiens.

PN WO200208259-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US023253.

PR 26-JUL-2000; 2000US-0220747P.

PA (ZYMO) ZYMOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

DR WPI; 2002-217048/27.

XX
XX

PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.

PS Disclosure; Page 101-102; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 *in vivo* by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for *in vivo* diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 variant degenerate coding sequence

SQ Sequence 2259 BP; 379 A; 234 C; 374 G; 293 T; 0 U; 979 Other;

Query Match	Score 104.6;	DB 6;	Length 2259;
	70.2%		

Matches 89; Conservative 26; Mismatches 34

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QY 61 TCGCAGCTGGCTGTGGCCCGCTGGCGGGTCCGGCCGCGGGCGCCGACCTGTGGC 120

Db 61 WSNCAR YTNCGNGTNGCNGCGGNGGWSNGGNMGNGCNGMGNGCNGAYACNTGYGNG 120


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QY 121 TCGAGGATGAAGCGGCTGCCCGACCCG 149
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ID ABA95032 standard; DNA; 2259 BP.
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AC ABA95032;
XX
DT 20-MAY-2002 (first entry)
XX
DE Human cytokine receptor, Zcytor18 degenerate coding sequence.
XX
KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; ds.
XX
OS Homo sapiens.
XX
FN WO200208259-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023253.
XX
PR 26-JUL-2000; 2000US-0220747P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Presnell SR, Kuestner RE, Gao Z;
XX
DR WPI; 2002-217048/27.
XX
DR P-PSDB; ABB07626.
XX
PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX
PS Disclosure; Page 92-93; 119pp; English.
XX
CC The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 degenerate coding sequence
XX
SQ Sequence 2259 BP; 379 A; 234 C; 373 G; 293 T; 0 U; 980 Other;

Query Match 70.2%; Score 104.6; DB 6; Length 2259;
Best Local Similarity 59.7%; Pred. No. 5.2e-16;
Matches 89; Conservative 26; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGCCCGTGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGCG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGGCNCCTGGTNCARVTNTGYWSNGTNTTYYACNGTNAAYGCTGYTNAAYGN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 TCGAGCTGGCTGGCGGCTCGCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
    ::|||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 61 WSNCARVTNGCTGNGCNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 TCGAGGATGAAGCGGCTGCCCGACCCG 149
    |||:| |||:| |||:| |||:| |||:| |||:| |||:|

```

RESULT 12
AA18135
ID AAS18135 standard; cDNA; 2214 BP.
XX
AC AAS18135;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DCRS8 reverse translation generic cDNA.
XX
KW Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; ss;
KW Gene therapy; protein therapy; immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200190358-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016767.
XX
PR 24-MAY-2000; 2000US-0206862P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM;
XX
DR WPI; 2002-106198/14.
XX
PT Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
PT useful for detecting antibodies generated in response to presence of
PT increased protein levels or immunological disorders.
XX
PS Disclosure; Page 25-26; 148pp; English.
XX
CC The invention relates to primate and rodent DNAX cytokine receptor
CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
CC receptors, or their portions may be useful as phosphate labelling enzymes
CC to label general or specific substrates. The subunits may also be
CC functional immunogens to elicit recognising antibodies, or antigens
CC capable of binding antibodies. A combination, e.g., including a DCRS can
CC be used as an immunogen for the production of antisera or antibodies
CC capable of distinguishing between other cytokine receptor family members.
CC A purified DCRS can also be used as a reagent to detect antibodies
CC generated in response to the presence of elevated levels of expression,
CC or immunological disorders which lead to antibody production to the
CC endogenous receptor. This sequence represents human DCRS8 reverse
CC translation generic cDNA
SQ Sequence 2214 BP; 371 A; 223 C; 358 G; 287 T; 0 U; 975 Other;
Query Match 56.1%; Score 83.6; DB 6; Length 2214;
Best Local Similarity 51.0%; Pred. No. 6e-11; Mismatches 0; Gaps 0;
Matches 74; Conservative 24; Indels 47; Indels 0; Gaps 0;
QY 1 ATGGCCCGCTGGCTGCAGCTCTGCTCGCTCTTCTTTACGCTCAACGCTCAACGGC 60
Db 1 ATGGCCNCCNTGGTTCARNTNTGWSNGTNTTTCACGCTCAACGCTCAACGGC 60
QY 61 TCGCAGCTGGCTGTGCGCGGTCTCGCGCGGTCTCGCGCGGTCTCGCGCGGTCTG 120
Db 61 WNCARYTNGCTGTCGCGCGGTCTCGCGCGGTCTCGCGCGGTCTCGCGCGGTCTG 120
QY 121 TCGAGGATGAACGCGCTGCCCGAC 145
Db 121 TCGNNNGTNGTNGCNCNCNWSNM 145
RESULT 13
AD123928
ID AD123928 standard; DNA; 18876 BP.
XX
AC AD123928;

RESULT 11
ABA95038
ID ABA95038 standard; DNA; 2217 BP.
XX
AC ABA95038;
XX
DT 20-MAY-2002 (first entry)
XX
DE Murine cytokine receptor, Zcytor18 degenerate coding sequence.
XX
KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
KW erythroleukemia; chromosome 3p14.3; gene therapy; mouse; ds.
XX
OS Mus sp.
XX
PN WO200208259-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023253.
XX
PR 26-JUL-2000; 2000US-0220747P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kuestner RE, Gao Z;
XX
DR WPI; 2002-217048/27.
XX
PS Disclosure; Page 118-119; 119pp; English.
XX
CC The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumor growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC murine Zcytor18 degenerate coding sequence
SQ Sequence 2217 BP; 362 A; 236 C; 365 G; 289 T; 0 U; 965 Other;
Query Match 58.9%; Score 87.8; DB 6; Length 2217;
Best Local Similarity 53.1%; Pred. No. 5.8e-12;
Matches 77; Conservative 26; Mismatches 42; Indels 0; Gaps 0;
QY 1 ATGGCCCGCTGGCTGCAGCTCTGCTCGCTCTTCTTTACGCTCAACGCTCAACGGC 60
Db 1 ATGGCCNCCNTGGTTCARNTNTGWSNGTNTTTCACGCTCAACGCTCAACGGC 60
QY 61 TCGCAGCTGGCTGTGCGCGGTCTCGCGCGGTCTCGCGCGGTCTCGCGCGGTCTG 120
Db 61 WNCARYTNGCTGTCGCGCGGTCTCGCGCGGTCTCGCGCGGTCTCGCGCGGTCTG 120
QY 121 TCGAGGATGAACGCGCTGCCCGAC 145
Db 121 TCGMNGGNGTNGCNCNCNWSNM 145

XX 22-APR-2004 (first entry)
 DT Streptomyces refuineus 024A locus ORF4.
 DE
 XX antimicrobial; fungicide; virucide; gene therapy; lipopeptide synthesis;
 KW A54145; NRRL 3143; antimicrobial; antifungal; antiviral;
 KW biosynthetic locus; 024A; ORF4; gene; ds.
 XX Streptomyces refuineus.
 OS
 XX US2003198981-A1.
 PN
 XX 23-OCT-2003.
 PD
 XX 24-DEC-2002; 2002US-00329079.
 PF
 XX 26-DEC-2001; 2001US-0342133P.
 PR
 XX 17-APR-2002; 2002US-0372789P.
 PR
 XX 03-SEP-2002; 2002US-00232370.
 PR
 XX (ECOP-) ECOPIA BIOSCIENCES INC.
 PA
 XX Farnet CM, Staffa A, Zazopoulos E;
 PI
 XX WPI; 2003-852784/79.
 DR
 XX P-PSDB; ADI23927.
 DR
 XX New isolated, purified or enriched nucleic acid, useful for synthesizing
 PT lipopeptides, particularly from the biosynthetic locus A54145 and NRRL
 PT 3143, that exhibits antimicrobial, antifungal or antiviral activity.
 PT
 XX Example 4; SEQ ID NO 42; 69pp; English.
 PS
 XX The invention describes an isolated, purified or enriched nucleic acid
 CC (1) comprising: any of 4 fully defined sequences (SEQ. ID NO: 1, 6, 17
 CC and 34), and their coding regions; a nucleic acid having at least 75%
 CC sequence identity to a nucleic acid of (a); or complements of (a) or (b).
 CC The methods and compositions of the present invention are useful for
 CC synthesizing lipopeptides, particularly A54145 and NRRL 3143, exhibiting
 CC antimicrobial, antifungal or antiviral activity. This sequence represents
 CC ORF4 of the Streptomyces refuineus 024A (or NRRL 3143) biosynthetic
 CC locus.
 XX
 SQ Sequence 18876 BP; 2128 A; 7584 C; 7023 G; 2141 T; 0 U; 0 Other;
 Query Match 27.9%; Score 41.6; DB 10; Length 18876;
 Best Local Similarity 55.6%; Pred. No. 0.89;
 Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 2 TGGCCCGGTGGCTGCGAGCTCTGCTCCGCTTTTACGGTCAACGCCCTGCTCAACGGCT 61
 Db 2636 TGGCGCAGCGCTGCTGACCGTGCAGGAACGGCGCGGCGACCGCAGGCTCGTCGGCT 2695
 QY 62 CCGAGCTGGCTGCGCGGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 121
 Db 2696 ACCTGGTCCCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 121
 QY 122 GGAGGATGAAGCGGCTGCCCGAC 145
 Db 2756 GCGGAGGCTGATCGCGCGCGCG 2779
 RESULT 14
 ADI23920
 ID ADI23920 standard; DNA; 61944 BP.
 XX
 AC ADI23920;
 XX
 DT 22-APR-2004 (first entry)
 DE Streptomyces refuineus 024A locus (NRRL 3143).
 XX

KW antimicrobial; fungicide; virucide; gene therapy; lipopeptide synthesis;
 KW A54145; NRRL 3143; antimicrobial; antifungal; antiviral;
 XX biosynthetic locus; 024A; ds.
 OS Streptomyces refuineus.
 PN US2003198981-A1.
 XX 23-OCT-2003.
 PD
 XX 24-DEC-2002; 2002US-00329079.
 PF
 XX 26-DEC-2001; 2001US-0342133P.
 PR
 XX 17-APR-2002; 2002US-0372789P.
 PR
 XX 03-SEP-2002; 2002US-00232370.
 PR
 XX (ECOP-) ECOPIA BIOSCIENCES INC.
 PA
 XX Farnet CM, Staffa A, Zazopoulos E;
 PI
 XX WPI; 2003-852784/79.
 DR
 XX New isolated, purified or enriched nucleic acid, useful for synthesizing
 PT lipopeptides, particularly from the biosynthetic locus A54145 and NRRL
 PT 3143, that exhibits antimicrobial, antifungal or antiviral activity.
 PT
 XX Claim 1; SEQ ID NO 34; 69pp; English.
 PS
 XX The invention describes an isolated, purified or enriched nucleic acid
 CC (1) comprising: any of 4 fully defined sequences (SEQ. ID NO: 1, 6, 17
 CC and 34), and their coding regions; a nucleic acid having at least 75%
 CC sequence identity to a nucleic acid of (a); or complements of (a) or (b).
 CC The methods and compositions of the present invention are useful for
 CC synthesizing lipopeptides, particularly A54145 and NRRL 3143, exhibiting
 CC antimicrobial, antifungal or antiviral activity. This sequence represents
 CC the Streptomyces refuineus 024A (or NRRL 3143) biosynthetic locus.
 XX
 SQ Sequence 61944 BP; 7372 A; 24375 C; 22809 G; 7388 T; 0 U; 0 Other;
 Query Match 27.9%; Score 41.6; DB 10; Length 61944;
 Best Local Similarity 55.6%; Pred. No. 0.95;
 Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 2 TGGCCCGGTGGCTGCGAGCTCTGCTCCGCTTTTACGGTCAACGCCCTGCTCAACGGCT 61
 Db 7696 TGGCGCAGCGCTGCTGACCGTGCAGGAACGGCGCGGCGACCGCAGGCTCGTCGGCT 7755
 QY 62 CCGAGCTGGCTGCGCGGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 121
 Db 7756 ACCTGGTCCCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 121
 QY 122 GGAGGATGAAGCGGCTGCCCGAC 145
 Db 7816 GCGGAGGCTGATCGCGCGCGCG 7839
 RESULT 15
 ACA26238/c
 ID ACA26238 standard; DNA; 567 BP.
 XX
 AC ACA26238;
 XX
 DT 19-JUN-2003 (first entry)
 DE
 XX Prokaryotic essential gene #7895.
 XX Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX Burkholderia mallei.
 OS
 XX WO200277183-A2.
 PN
 XX

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Result No.	Score	Query			DB	ID	Description
		Match	Length				
C 1	38	25.5	2262	4	US-09-949-016-5805	Sequence 5805, Ap	
C 2	38	25.5	84870	4	US-09-949-016-17547	Sequence 17547, Ap	
C 3	37.8	25.4	72704	4	US-09-902-540-1273	Sequence 1273, Ap	
5	36.6	24.6	50109	4	US-09-949-016-14112	Sequence 14112, Ap	
	35.6	23.9	1674	4	US-09-252-991A-1645	Sequence 1645, Ap	
	35.6	23.9	1785	4	US-09-252-991A-1528	Sequence 1528, Ap	
C 6	35.6	23.9	1785	4	US-09-252-991A-1528	Sequence 1528, Ap	
C 7	34.4	23.1	1437	4	US-09-902-540-3148	Sequence 3148, Ap	
C 8	34.4	23.1	19598	4	US-09-902-540-1143	Sequence 1143, Ap	
C 9	34.2	23.0	531	4	US-09-252-991A-8317	Sequence 8317, Ap	
C 10	34.2	23.0	1092	4	US-09-252-991A-14341	Sequence 14341, Ap	
C 11	34.2	23.0	1167	4	US-09-252-991A-14278	Sequence 14278, A	
C 12	34.2	23.0	1332	1	US-08-660-765A-3	Sequence 3, Appli	
C 13	34.2	23.0	94156	4	US-09-949-016-12388	Sequence 12388, A	
C 14	34.2	23.0	102406	4	US-09-949-016-14673	Sequence 14673, A	
C 15	33.8	22.7	1494	4	US-09-902-540-6461	Sequence 6461, Ap	
C 16	33.8	22.7	1664	4	US-09-902-540-452	Sequence 452, App	
C 17	33.8	22.7	3126	3	US-09-392-184-7	Sequence 7, Appli	
C 18	33.6	22.6	1455	4	US-09-489-039A-4834	Sequence 4834, Ap	
C 19	33.4	22.4	603	4	US-09-252-991A-5926	Sequence 5926, Ap	
C 20	33.4	22.4	1461	4	US-09-252-991A-5911	Sequence 5911, Ap	
C 21	33.4	22.4	2796	4	US-09-252-991A-5979	Sequence 5979, Ap	
C 22	33.2	22.3	22761	4	US-09-902-540-1219	Sequence 1219, Ap	
C 23	33	22.1	2558	4	US-09-902-540-6342	Sequence 6342, Ap	
C 24	33	22.1	2560	4	US-09-902-540-400	Sequence 400, App	
C 25	32.8	22.0	468	4	US-09-252-991A-3702	Sequence 3702, Ap	
C 26	32.8	22.0	513	4	US-09-252-991A-3811	Sequence 3811, Ap	
C 27	32.8	22.0	744	4	US-09-252-991A-3651	Sequence 3651, Ap	

;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 17547
;; LENGTH: 84870
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)-(84870)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17547

Query Match 25.5%; Score 38; DB 4; Length 84870;
Best Local Similarity 58.2%; Pred. No. 1.5;
Matches 85; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 3 GGCCCGGTGGTGGAGCTGCTGCTCTTTTACGGTCAAGCGCTGCCTCAACGGCTC 62
DB 2212 GGACATGGTGTGCTGCTCTCTGCTGCGCATCTCTCACTCCCGCGCTCAAC-GCTG 2154

QY 63 CGACGTGGCTGGCGCTGGCGGTCCGCGCGCGGGCGCGGCGGACACTGTGGCTG 122
DB 2153 GAGCGCGGGGTGGCGGGGGGGGCTTCGGGCGCGGCGGACTCCGCGCGCTGCGCTG 2094

QY 123 GAGGATGAAGCGGTGCGCGGACCC 148
DB 2093 CCGGAGACCGCGGCGCTCGGCCAC 2068

RESULT 3
US-09-902-540-1273/c
; Sequence 1273, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1273
; LENGTH: 72704
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72704)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273

Query Match 25.4%; Score 37.8; DB 4; Length 72704;
Best Local Similarity 55.8%; Pred. No. 1.6;
Matches 72; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 21 CTGCTCCGCTCTTTTACGGTCAACGCTGCCTCAACGGCTGCAGCTGGCTGTGGCGCG 80
DB 24848 CAGCCCTTGTGTCACGGCGCGCGGACAGCGCGAGCTCTCGCAGAAGCGCGGGTGT 24789

QY 81 TGGCGGGTCCGCGCGCGCGGGCGCGGACACTGTGCTGGAGGATGAAGCGGCTGC 140

DB 24788 CAGCGGCTCCCTCCATGCCAGCGCGGCGCTTGCGGAAGCGCGCGCGCGCGG 24729
QY 141 CCGACCCCG 149
DB 24728 CGCACACG 24720

RESULT 4

US-09-949-016-14112
; Sequence 14112, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14112
; LENGTH: 50109
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)..(50109)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14112

Query Match 24.6%; Score 36.6; DB 4; Length 50109;
Best Local Similarity 60.6%; Pred. No. 3.1;
Matches 60; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 12 GCTCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGCTGCCTCAACGGCTGCAGCTGGC 71
DB 2069 GCTGAACCTGCGCGCGCTCTTCGATGCAACAGAGCGCTTCAACCACTTCAGTGGCG 2128

QY 72 TGTGCGCGCTGCGGGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 110
DB 2129 CGCGGCGGAGCGGGGCTGCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2167

RESULT 5

US-09-252-991A-1645
; Sequence 1645, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1645
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1645

Query Match 23.9%; Score 35.6; DB 4; Length 1674;

Best Local Similarity 64.6%; Pred. No. 4.3;
Matches 53; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 33 CTTTACGGTCAACGGCTGCTCAACGGCTCGAGCTGGCTGGCGGCTGGCGGCTCGG 92
Db 1203 CTTCTCTGGTCAAGCGCGGCTGCTTACTCGACGGTGGCGCGCGCGGCGGACGT 1262

QY 93 CGCGCGCGCGCGCGCGACACC 114
Db 1263 CAGGTGCGGATCGGCGAGACC 1284

RESULT 6
US-09-252-991A-1528/c
; Sequence 1528, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1528
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1528

Query Match 23.9%; Score 35.6; DB 4; Length 1785;
Best Local Similarity 64.6%; Pred. No. 4.3;
Matches 53; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 33 CTTTACGGTCAACGGCTGCTCAACGGCTCGAGCTGGCTGGCGGCTGGCGGCTCGG 92
Db 535 CTTCTCTGGTCAAGCGCGGCTGCTTACTCGACGGTGGCGCGCGCGCGGACGT 476

QY 93 CGCGCGCGCGCGCGCGACACC 114
Db 475 CAGGTGCGGATCGGCGAGACC 454

RESULT 7
US-09-902-540-3148/c
; Sequence 3148, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3148
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3148

Query Match 23.1%; Score 34.4; DB 4; Length 1437;
Best Local Similarity 52.9%; Pred. No. 8.5;
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGGCCCGCTGGCTCGAGCTGTGCTCCGTCTTTTACGGTCAACGGCTGCTCAACGGC 60
Db 380 AAGGCCACGTTGAGGAGCGGAGGAGTAGTTCCGCTCCAGGTTTCCGCCAGTTGG 321

QY 61 TGCAGCTGGCTGTGGCGGCTGGCGGCTCCGCGCGCGCGCGCGCGGACCTGTGGC 120
Db 320 AAGAGCGCGCGCGCGCGCGCTTCCACGGCGCGCGCGCGCGCGGACCTTCCACCGGGAAG 261

QY 121 TGGAGGATCAAGACGGCTGC 140
Db 260 AGGAGGAAGCACACGGCGC 241

RESULT 8
US-09-902-540-1143
; Sequence 1143, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1143
; LENGTH: 19598
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(19598)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1143

Query Match 23.1%; Score 34.4; DB 4; Length 19598;
Best Local Similarity 52.9%; Pred. No. 10;
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGGCCCGCTGGCTCGAGCTGTGCTCCGTCTTTTACGGTCAACGGCTGCTCAACGGC 60
Db 14162 AAGGCCACGTTGAGGAGCGGAGGAGTAGTTCCGCTCCAGGTTTCCGCCAGTTGG 14221

QY 61 TGCAGCTGGCTGTGGCGGCTGGCGGCTCCGCGCGCGCGCGCGGACCTGTGGC 120
Db 14222 AAGAGCGCGCGCGCGCGCTTCCACGGCGCGCGCGCGCGGACCTTCCACCGGGAAG 14281

QY 121 TGGAGGATCAAGACGGCTGC 140
Db 14282 AGGAGGAAGCACACGGCGC 14301

RESULT 9
US-09-252-991A-8317/c
; Sequence 8317, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8317


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; LENGTH: 531
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8317

Query Match          23.0%; Score 34.2; DB 4; Length 531;
Best Local Similarity 55.5%; Pred.No. 8.9; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 53;

Qy 15 GCAGCTCTGCTCCGCTCTTTTACGGTCAACGGCTGCCTCAACGGCTCGCAGCTGGCTGT 74
Db 220 GCTGCACCGCTTTGTTTTCGGAACGGCGCATGGCTTGTCTCGGCTGCCTCCACCTGGGCT 161
Qy 75 GCGCGCTGGCGGGTTCGGCCGCGCGGGCGCGCACCTGTGGCTGGAGGATGAAAG 133
Db 160 GGCTGTGCGGCAGGCTGTCTCGGAGCAGGCGCGGGTATCAGCGGGTTTCGGCTGGACG 102

RESULT 10
US-09-252-991A-14341/c
; Sequence 14341, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14341
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14341

```

	Query Match	23.0%;	Score 34.2;	DB 4;	Length 1092;	
	Best Local Similarity	55.5%;	Pred. No. 9.3;			
	Matches	66;	Conservative 0;	Mismatches 53;	Indels 0;	Gaps 0;
Qy	6	CCCGTGGCTCGAGCTTCGCTCGTGTTCTTTACGGTCAACGCCTGCCTCAACGGCTGCGA	65			
Dd	907	CCTGGTGACGCTCCAGGTCAACCGCGTGTGATGCTCTTCGGCATCCTCATGCCCTGCT	848			
Qy	66	GCTGGCTGTGGCCGCTCGCGGGTTCGGCCCGGCGCGGGGCCGACACTGTGTGGCTGGA	124			
Dd	847	CCTGGCTCTCGCCCGGCTCGCGCGGTAAACGCCCGCTGCGCGCGCGCCGAGACCTTGA	789			

RESULT 11
 US-09-252-991A-14278
 Sequence 14278, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 14278
 LENGTH: 1167
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa

```

US-09-252-991A-14278

Query Match      23.0%; Score 34.2; DB 4; Length 1167;
Best Local Similarity 55.5%; Pred.No.9.4;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY      6  CCGTGGCTCAGCTGCTGCTCCGCTCTTTTACGGTCAACGCCCTGCTCAACGGCTCGCA 65
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      567 CTTGGTACGCTCAGGTCAACCGGCTGTGTGATGCTCTTGGCATCCTCATCGCCCTGCT 626
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      66  GCTGGCTGTGGCGGCTGGCGGGTCCGCGCGCGGGGGCGCCGACACCTTGTGGCTGSA 124
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      627 CTTGGCTTCCGCCGGCTCGCGGTGAACGCCCGCTGCGCGCGCGGAGCTGSA 685
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-08-660-765A-3/c
; Sequence 3, Application US/08660765A
; Patent No. 5652125
; GENERAL INFORMATION:
; APPLICANT: SCOTTI, Claudio
; APPLICANT: HUTCHINSON, Charles R.
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: FILIPPINI, Silvia
; TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; STREET: Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,765A
; FILING DATE: 10-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERMAN, Richard J.
; REGISTRATION NUMBER: 39,107
; REFERENCE/DOCKET NUMBER: P1615-6005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1332 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-660-765A-3

```

Query Match	23.0%;	Score 34.2;	DB 1;	Length 1332;
Best Local Similarity	56.8%;	Pred. No. 9.5;		
Matches	63;	Conservative 0;	Mismatches 48;	Indels 0; Gaps 0;
Qy	1	ATGGCCCCGTGGCTGCGAGCTGCTCCGTCTTCTTTACGGTCAACGGCTGCGCTCAACGGC	60	
Db	602	ATGTCCCCCGGCTCGCGCCGACCGCTCCACGCTCCAGGTGAGCCACTCGGCCAGCGGG	543	
Qy	61	TCGCAGCTGCGTGTGCGCGCTGGCGGGTCCGGCCCGCGGGCGGGCGCGAC	111	
Db	542	TCGTCCGGCAGCTCGGGCGGTTCGGGTTCGAGCAGGGCGCGGAACGCCGTC	492	
RESULT 13				

```
US-09-949-016-12388/c
; Sequence 12388, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12388
; LENGTH: 94156
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(94156)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12388

Query Match      23.0%; Score 34.2; DB 4; Length 94156;
Best Local Similarity 56.8%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 39 GGTCAACGCTGCTCAACGGCTCGAGCTGCTGTGCGCGGTGCGGGTCCGGCGCGC 98
DB 30991 GGTCAACGCTGCTCAACGGCTCGAGCTGCTGTGCGCGGTGCGGGTCCGGCGCGC 30932

QY 39 GGTCAACGCTGCTCAACGGCTCGAGCTGCTGTGCGCGGTGCGGGTCCGGCGCGC 98
DB 30991 GGTCAACGCTGCTCAACGGCTCGAGCTGCTGTGCGCGGTGCGGGTCCGGCGCGC 30932

QY 99 GCGGGGCGCGCACACCTGTGGCTGGAGGATGAAAGCGGTGCGCGCGCGC 149
DB 30931 CCGGCCAGCGCGCCCTGTCGGGAGGAGGTGCGGGGCGTCAAGCGCGCGC 30881

RESULT 14
US-09-949-016-14673/c
; Sequence 14673, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14673
; LENGTH: 102406
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(102406)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14673

Query Match      23.0%; Score 34.2; DB 4; Length 102406;
Best Local Similarity 56.8%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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QY 39 GGTCAACGCTGCTCAACGGCTCGAGCTGCTGTGCGCGGTGCGGGTCCGGCGCGC 98
DB 30991 GGTCAACGCTGCTCAACGGCTCGAGCTGCTGTGCGCGGTGCGGGTCCGGCGCGC 30932

QY 99 GCGGGGCGCGCACACCTGTGGCTGGAGGATGAAAGCGGTGCGCGCGCGC 149
DB 30931 CCGGCCAGCGCGCCCTGTCGGGAGGAGGTGCGGGGCGTCAAGCGCGCGC 30881

RESULT 15
US-09-902-540-6461
; Sequence 6461, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6461
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(1494)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-6461

Query Match      22.7%; Score 33.8; DB 4; Length 1494;
Best Local Similarity 58.4%; Pred. No. 12;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 2 TCGCCCCGTGGCTGCGAGCTGCTCGGCTTTCTTTACGGTCAACGCTCGCTCAACGGCT 61
DB 512 TGGACCGGGTGTGCGCGCGCGCTTCGGCGACTGCAAGGACAAAGGCGAGCTCATCACT 571

QY 62 CGCAGCTGGCTGTGCGCGCTGCGGGTCCGGCGCGCGCGCGG 102
DB 572 CCATGCTCCAGTGGCGGGTGGAGAGCGCGCTGGTGTG 612

Search completed: August 16, 2005, 05:24:24
Job time : 145 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: August 16, 2005, 03:47:42 ; Search time 3171 Seconds
(without alignments)
1788.577 Million cell updates/sec

Title: US-10-717-282-1_COPY_86_234
Perfect score: 149
Sequence: 1 atggcccgctggctgcagct.....aaagcggtgccgaccccg 149

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsal:*
9: gb_gsal2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126.8	85.1	585	4	BG149830 nae01a12
2	125	83.9	230	2	BP515598 UT-H-BW1
3	112.6	75.6	474	6	CAB79041 K0971D08
4	112.6	75.6	665	2	BB641245 BB641245
5	111.6	74.9	239	8	CC178870 XST163 Ba
6	110	73.8	547	2	BE750478 201867 MA
7	101.8	68.3	483	5	BY152713 BY152713
8	99.8	67.0	724	5	BP154750 BP154750
9	51.6	34.6	134	9	CL212737 G049F09 G
10	43.6	29.3	271	1	AL450535 AL450535
11	43	28.9	573	4	BM371103 EBr004 SQ
12	43	28.9	854	2	BF630932 HVSMB001
13	41.8	28.1	513	7	CF260435 NC-EST3d04
14	41.8	28.1	565	7	CF943197
15	41.8	28.1	565	7	CF261081 NC-EST3c80
16	40	26.8	533	6	CA259967 SCPRRT302
17	38.8	26.0	313	5	BQ753596 EBan01 SQ
18	38.8	26.0	454	5	BQ764296 EBan01 SQ
19	38.8	26.0	591	5	BQ764291 EBan01 SQ
20	38.6	25.9	622	7	CN412349
21	38.4	25.8	676	6	CD058409 H0040228
22	38	25.5	366	7	CN412348
23	38	25.5	555	7	CN412341
24	38	25.5	599	4	BG720080 602691584

C 25	38	25.5	656	7	CN412342
C 26	38	25.5	666	7	CN412351
C 27	38	25.5	710	7	CN412352
C 28	38	25.5	800	4	BG718697
C 29	38	25.5	916	5	BU509388
C 30	38	25.5	1001	2	BE783051
C 31	38	25.5	2088	9	CL507788
C 32	37.8	25.4	398	8	AZ047386
C 33	37.8	25.4	526	4	BI562240
C 34	37.8	25.4	529	1	AL829621
C 35	37.8	25.4	811	9	CG660832
C 36	37.6	25.2	332	1	AJ679503
C 37	37.6	25.2	626	6	CA149067
C 38	37.4	25.1	542	9	CL793216
C 39	37.4	25.1	603	9	CL774375
C 40	37.4	25.1	775	4	BG610752
C 41	37.4	25.1	1036	7	CK213161
C 42	37.2	25.0	277	1	AU177782
C 43	37.2	25.0	319	1	AV939902
C 44	37.2	25.0	478	5	BU970198
C 45	37.2	25.0	487	5	BU970159

ALIGNMENTS

RESULT 1
BG149830 nae01a12.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3434014 3', linear EST 30-MAR-2001
LOCUS mRNA sequence.
DEFINITION BG149830.1 GI:12661860
ACCESSION BG149830
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 585)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Cloned through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 492.
Location/Qualifiers
1. 585
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3434014"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
/note="Organ: ovary; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCACATCTGAAGTGGAGCGCGCGGACATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

CGAP is a project of the National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Cloned through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 492.
Location/Qualifiers
1. 585
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3434014"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
/note="Organ: ovary; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCACATCTGAAGTGGAGCGCGCGGACATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuhiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsueura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Konodo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

```

1. .665
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A830013G13"
/tissue_type="cortex"
/dev_stage="10 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 10 days neonate
cortex"
note="Site 1: Sali; Site 2: BamHI; cDNA library was

```

GAGAGAGAGAGAGATCCAGAGACTCTTTTCTTTTCTTTTCTTN 3', cDNA was prepared by using trisphosphate thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATCTCGATTAAATTAATGCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda phage. FIG. 1."

[illegible]

Qy	61	TCACAGTGGCTGTGACCGGTGGCGGCTCCGGCCGCGCGCGGCGCGGACACCTGTGGC	121
Db	93	TCACAGCTGGCAGTGGCCGCGGCGGGGCTCCGGCCGCGGAGGGGCGGACACCTGTGGC	152
Qy	121	TGGAGGATGAAGCGCGTGTCCCG	143
Db	153	TGGAGGGGAGTGGGGCGCGCCAG	175

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RESULT 5
CC178870
LOCUS      XST163 BayGenomics Gene Trap Library pGrlTWpfs Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION CC178870
VERSION    CC178870.1 GI:30317421
KEYWORDS   Mus musculus (house mouse)
SOURCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 239)
AUTHORS     BayGenomics.
TITLE       http://baygenomics.ucsf.edu/
JOURNAL     Unpublished (2001)
COMMENT     Contact: BayGenomics
            Bay Area Functional Genomics Consortium (BayGenomics)
            Email: info@baygenomics.ucsf.edu
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from BayGenomics. Annotation
            information available from
            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
            CELL_LINE&KEY=XST163
FEATURES
            Class: Gene trap.
            Location/Qualifiers
                1..239
                 /organism="Mus musculus"
                 /mol_type="mRNA"
                 /strain="129 ola"
                 /db_xref="taxon:10090"
                 /sex="Male"
                 /cell_type="Embryonic stem cell"
                 /clone_lib="BayGenomics Gene Trap Library pGrlTWpfs"
                 /note="Vector: pGrlTWpfs"
ORIGIN
Query Match      74.9%; Score 111.6; DB 8; Length 239;
Best Local Similarity 92.9%; Pred. No. 1.6e-17;
Matches 117; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY      1 ATGGCCCGTGGCTGCAGCTCTGCTCGCTCTCTTTACGGTCAACGCTGCTCAACGGC 60
        |||||
        114 ATGGCCCGTGGCTGCAGCTCTGCTCGCTCTCTTTACCTGTCAACGCTGCTCAACGGC 173
        |||||
QY      61 TCGCAGCTGGCTGGCGGCTCGCGGGTCCGGCCGCGCGCGCGCGCGACACCTGTGGC 120
        |||||
        174 TCGCAGCTGGCAGTGGCGCGGGTCCGGCCGCGCGCGCGCGCGACACCTGTGGC 233
        |||||
QY      121 TGGAGG 126
        |||||
        234 TGGAGG 239
        |||||
RESULT 6
BE750478
LOCUS      201867 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BE750478
ACCESSION  BE750478
VERSION     BE750478.1 GI:10164470
KEYWORDS    Bos taurus (cow)
SOURCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1 (bases 1 to 547)
AUTHORS     Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
            Casas, E., Wray, J.E., White, J., Cho, J., Fahrnenkrug, S.C.,
            Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
            Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
            Quackenbush, J. and Keele, J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
            11280013
            11282978
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smithemail.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCCAGTCACGACG
            Plate: 112 row: C column: 10
            Seq primer: ATTTAGGTGACACTATAG.
            Location/Qualifiers
                1..547
                 /organism="Bos taurus"
                 /mol_type="mRNA"
                 /db_xref="taxon:9913"
                 /tissue_type="pooled"
                 /lab_host="DH10B"
                 /clone_lib="MARC 4BOV"
                 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                 Library made from pooled tissue from day 20 and day 40
                 embryos."
ORIGIN
Query Match      73.8%; Score 110; DB 2; Length 547;
Best Local Similarity 92.1%; Pred. No. 4e-17;
Matches 116; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      1 ATGGCCCGTGGCTGCAGCTCTGCTCGCTCTCTTTACGGTCAACGCTGCTCAACGGC 60
        |||||
        17 ATGGCCCGTGGCTGCAGCTCTGCTCGCTCTCTTTACGGTCAACGCTGCTCAACGGT 76
        |||||
QY      61 TCGCAGCTGGCTGGCGGCTGGCGGGTCCGGCCGCGCGCGCGCGACACCTGTGGC 120
        |||||
        77 TCGCAGCTGGCGGCTGGCTGGCGGGTCCAGAGAGCGCGCGCGCGACACCTGTGGC 136
        |||||
QY      121 TGGAGG 126
        |||||
        137 TGGAGG 142
        |||||
RESULT 7
BY152713
LOCUS      BY152713 RIKEN full-length enriched, B16 F10Y cells Mus musculus
DEFINITION cDNA clone G370032A13 5', mRNA sequence.
ACCESSION  BY152713
VERSION     BY152713.1 GI:26289242
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 483)
            Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
            Nikaado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
            Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
            Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
            Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
            Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
            Chotha, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A.,
            Flatcher, C., Forrest, A., Frazer, K.S., Gaasterland, T.,
            Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
            Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
            Quackenbush, J. and Keele, J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
            11280013
            11282978
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smithemail.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCCAGTCACGACG
            Plate: 112 row: C column: 10
            Seq primer: ATTTAGGTGACACTATAG.
            Location/Qualifiers
                1..547
                 /organism="Bos taurus"
                 /mol_type="mRNA"
                 /db_xref="taxon:9913"
                 /tissue_type="pooled"
                 /lab_host="DH10B"
                 /clone_lib="MARC 4BOV"
                 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                 Library made from pooled tissue from day 20 and day 40
                 embryos."
ORIGIN
Query Match      73.8%; Score 110; DB 2; Length 547;
Best Local Similarity 92.1%; Pred. No. 4e-17;
Matches 116; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      1 ATGGCCCGTGGCTGCAGCTCTGCTCGCTCTCTTTACGGTCAACGCTGCTCAACGGC 60
        |||||
        17 ATGGCCCGTGGCTGCAGCTCTGCTCGCTCTCTTTACGGTCAACGCTGCTCAACGGT 76
        |||||
QY      61 TCGCAGCTGGCTGGCGGCTGGCGGGTCCGGCCGCGCGCGCGCGACACCTGTGGC 120
        |||||
        77 TCGCAGCTGGCGGCTGGCTGGCGGGTCCAGAGAGCGCGCGCGCGACACCTGTGGC 136
        |||||
QY      121 TGGAGG 126
        |||||
        137 TGGAGG 142
        |||||
RESULT 7
BY152713
LOCUS      BY152713 RIKEN full-length enriched, B16 F10Y cells Mus musculus
DEFINITION cDNA clone G370032A13 5', mRNA sequence.
ACCESSION  BY152713
VERSION     BY152713.1 GI:26289242
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 483)
            Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
            Nikaado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
            Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
            Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
            Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
            Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
            Chotha, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A.,
            Flatcher, C., Forrest, A., Frazer, K.S., Gaasterland, T.,
            Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
            Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
            Quackenbush, J. and Keele, J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
            11280013
            11282978
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smithemail.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCCAGTCACGACG
            Plate: 112 row: C column: 10
            Seq primer: ATTTAGGTGACACTATAG.
            Location/Qualifiers
                1..547
                 /organism="Bos taurus"
                 /mol_type="mRNA"
                 /db_xref="taxon:9913"
                 /tissue_type="pooled"
                 /lab_host="DH10B"
                 /clone_lib="MARC 4BOV"
                 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                 Library made from pooled tissue from day 20 and day 40
                 embryos."
ORIGIN
Query Match      73.8%; Score 110; DB 2; Length 547;
Best Local Similarity 92.1%; Pred. No. 4e-17;
Matches 116; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      1 ATGGCCCGTGGCTGCAGCTCTGCTCGCTCTCTTTACGGTCAACGCTGCTCAACGGC 60
        |||||
        17 ATGGCCCGTGGCTGCAGCTCTGCTCGCTCTCTTTACGGTCAACGCTGCTCAACGGT 76
        |||||
QY      61 TCGCAGCTGGCTGGCGGCTGGCGGGTCCGGCCGCGCGCGCGCGACACCTGTGGC 120
        |||||
        77 TCGCAGCTGGCGGCTGGCTGGCGGGTCCAGAGAGCGCGCGCGCGACACCTGTGGC 136
        |||||
QY      121 TGGAGG 126
        |||||
        137 TGGAGG 142
        |||||

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Db      158 TGGAGGGAGTGGGGCCGCCAG 180
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CL212737 134 bp mRNA linear GSS 30-JUN-2004
LOCUS     G049F09 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
DEFINITION G049F09, mRNA sequence.
ACCESSION CL212737
VERSION    CL212737.1 GI:40729638
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 134)
Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,P.,
Arnold,H.H., Schutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
JOURNAL   12904583
MEDLINE   22810117
PUBMED    12904583
COMMENT   Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
U3CEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=G049F09'. ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 16755
Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1..134
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="G049F09"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"
/clone_lib="GGTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"

ORIGIN
Query Match 34.6%; Score 51.6; DB 9; Length 134;
Best Local Similarity 70.3%; Pred. No. 0.012;
Matches 83; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

Qy 1 ATGGCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGGCTCGCTCAACGGC 60
|||||
Db 15 ATGGAACAGTGGATGCAGTTTCGATCAATATCTTCAATG-AAAACCCCTCTCGTAGT 73
|||||

Qy 61 TGGCAGCTGGCTGTGCCGCTGGCGGGTCCGGCCCGCGCGGGCGCGACACCTGTG 118
|||||
Db 74 TGGCAGCTGACAGTGGCCGCGAGCGCTCCGCCCGCGCGGGCGCGACACCTGGG 131
|||||

RESULT 10
AL450535 271 bp mRNA linear EST 07-DEC-2000
LOCUS     AL450535 Hordeum vulgare Barke etiolated leaves Hordeum vulgare
DEFINITION subsp. vulgare cDNA clone HK03A19u 5', mRNA sequence.
ACCESSION AL450535
VERSION    AL450535.1 GI:11601943
KEYWORDS  EST.
SOURCE    Hordeum vulgare subsp. vulgare
ORGANISM  Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 271)
Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: M13uni primer for 5'end.
Location/Qualifiers
1..271
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HK03A19u"
/tissue_type="etiolated leaves"
/lab_host="XL1Blue"
/clone_lib="Hordeum vulgare Barke etiolated leaves"
/note="Vector: pBluescript SK-; Site.1: SalI; Site.2:
NotI; mRNA was made from etiolated leaves of spring barley
variety 'Barke', a high quality malting variety. Plants
were grown on filterpaper for 6 d at 25 C in the dark.
Leaves were harvested at daylight conditions. Sal-Adaptor
Sequence: TCGACCCAGGCGTCG Average insert size is 1 kb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
set to 700 bp."

ORIGIN
Query Match 29.3%; Score 43.6; DB 1; Length 271;
Best Local Similarity 60.9%; Pred. No. 1.1;
Matches 70; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 4 GCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGGCTCGCTCAACGGCTCG 63
|||||
Db 65 GGCCCGCGGCTGCGCGCGGCCCTCTCGCTCGCCCCACCGCGGGCTCTCCGGCCCC 124
|||||

Qy 64 CAGCTGGCTGTGGCGGCTGGCGGGTCCGGCCCGCGCGGGCGCGACACCTGTG 118
|||||
Db 125 GAGCAAGATGTCGCTCGGTGAAGGCGCGCGGAGCTGGCGCGCGCTG 179
|||||

RESULT 11
BM371103 573 bp mRNA linear EST 23-JUL-2002
LOCUS     BM371103 Hordeum vulgare subsp. vulgare cDNA clone EBR04_SQ003_H20 5', mRNA
DEFINITION subsp. vulgare subsp. vulgare salt-stressed, cv Optic, EBR04
sequence.
ACCESSION BM371103
VERSION    BM371103.2 GI:21949377
KEYWORDS  EST.
SOURCE    Hordeum vulgare subsp. vulgare
ORGANISM  Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 573)
Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardie,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Jan 10, 2002 this sequence version replaced gi:18114493.
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426

```

Email: est@cri.sari.ac.uk
 All sequence has a Phred quality score of 20 or over
 Seq primer: M13 reverse.
 Location/Qualifiers
 source 1..573

FEATURES

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1. 1573
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBRo04_SQ003_H20"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_l1b="root, 3 week, salt-stressed, cv Optic."EBRo04"
/notes="Vector: pSPORt1; Site 1: Sal I; Site 2: Not I.
Non-normalised library, directionally cloned into pSPORt1.
Derived from roots of 3 week old salt stressed barley
plants. Developed as part of the barley transcriptome
resources of BBSC/SEBRAD funded cereal IGF (Investigating
Gene Function) project."

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ORIGIN

	Query Match	28.9%	Score 43	DB 4	Length 573
	Best Local Similarity	60.9%	Pred. No. 1.5		
	Matches	70	Conservative	0	Mismatches 45
					Indels 0
					Gaps 0
Qy	4	GCCCCGTGGCTGAGCTCTGCTGGTCTTTTACGGTCAACGGCTGCCTCAACGGGTGCG	63		
Db	14	GGCCCCGGGTGGCGCGGGCGCCCTCGCGCTGCCCCACCGCGCGCTCTCGGCCCC	73		
Qy	64	CAGTGGCTGTGGCCGCTGGGGGTCTGGCGCGCGGGCGCCGACACCTGTG	118		
Db	74	GAGCAAGATGTCGCCCTCGGTGAAGCGGGGGACCGCGGAGTGTGGCGGCGTG	128		

RESULT	12
LOCUS	BFB30932
FEATURES	
DEFINITION	BFB30932 854 bp mRNA linear EST 22-OCT-2001 HVSMB00014H1f Hordeum vulgare seedling shoot EST library HYCDNA0002 (Dehydration stress) Hordeum vulgare subsp. vulgare cDNA clone HVSMEB00014H1f, mRNA sequence.
ACCESSION	BFB30932
VERSION	BFB30932.2 GI:13091792
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. vulgare
ORGANISM	Hordeum vulgare subsp. vulgare
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum. 1. (bases 1 to 854) Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D. Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA library
TITLE	
JOURNAL	Unpublished (2001)
COMMENT	On Dec 19, 2000 this sequence version replaced gi:11895090.

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: wing@clemson.edu
Total hg bases = 432
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 526.
Location/Qualifiers

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FEATURES
source
location/Qualifiers
1..854
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mrna"

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/cultivar="Worex"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="HVSMEb0014H11f"
 /tissue_type="Seedling shoot"
 /lab_host="TJC121"
 /clone_lib="Hordeum vulgare seedling shoot EST library
 HVCDNA0002 (Denydration stress)"
 /notes="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 90% RH for 24 hr. Shoots were then harvested, one
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, 600000 pfu were
 in vivo excised to give bluescript SK(-) cDNA phagemids.
 These steps were performed in the TJ Close laboratory at
 the University of California, Riverside (Choi, Close,
 Fenton). Phagemids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
<http://wheat.rw.usda.gov/canages/ban/31/cover.html>"

ORIGIN

	Query Match	28.9%	Score 43;	DB 2;	Length 854;
	Best Local Similarity	60.9%	Pred. No. 1.5;		
	Matches	70;	Conservative	0;	Mismatches 45; Indels 0; Gaps 0
Qy	4	GCCCGTGGTGAGCTCTGCTCGTCTTTCTTTACGCTCAACGCTCGCTCTCAACGGCTCG	63		
Db	29	GGCCCGCGGTGGCGCGCGCCCTCGCGTGGCCCCACCGCGCGCGTCTCGCGCCCC	88		
Qy	64	CAGCTGGCTGTGCCCGGTGCGGGGTCCGGCGCGCGCGGGCGCGCACACTGTG	118		
Db	89	GAGCAAGATGTCCCTCTCGTGAAGGCGCGGACCGCGCGAGCTGGCGCGCTG	143		

RESULT	13
CF260435/c	
LOCUS	
DEFINITION	
ACCESSION	CF260435
VERSION	NCBI-1987
KEYWORDS	CDNA 5' end, mRNA sequence.
SOURCE	Neospora caninum
ORGANISM	Neospora caninum
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Neospora. 1 (bases 1 to 513) Cole, R., Fogarty, S., Tang, X., Howe, D.K., Sibley, L.D., Clifton, S., Marras, M., Hillier, B., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Teagareishvili, R., Fedele, M., Belaygorod, L., Franklin, C., Carr, L.M., Grow, A., Maguire, L., Wadkins, J., Richey, J., Waterston, R. and Wilson, R.
TITLE	USDA-WashU Neospora EST Project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Sandy Clifton, Ph.D. - Neospora USDA-WashU Neospora EST project Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Contact David Sibley (toxostest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: T3
High quality sequence stop: 509.

FEATURES

```

1. .513
location, quadrants
/organism="Neospora caninum"
/mol_type="mRNA"
/db_xref="taxon:29176"
/dev_stage="Tachyzoite"
/lab_host="Electrofen Blue cells (Stratagene)"
/clone_lib="NC-LIV Tachyzoite cDNA Library"
/notes=vector: pBluescript II SK+vector.type: plasmid;
Site_1: EcoRI; Site 2: XhoI; The cDNA library was
constructed by Kellang Tang, and Robert Cole at Washington
University. cDNA was synthesized from Poly(A)+ mRNA using
an oligo-(dT) primer containing a XhoI site. Following
second strand synthesis, EcoRI adapters were ligated to
the cDNA, and products were size-selected on sephacryl
S500. The cDNA were directionally cloned into the
EcoRI/XhoI prepared pBluescript II SK+ vector, and
electroporated into Electrofen Blue cells (Stratagene).
The library may contain a small percentage of host or
bacterial contaminants."

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ORIGIN

Query Match	28.1%;	Score 41.8;	DB 7;	Length 513;
Best Local Similarity	65.6%;	Pred. No. 2.9;		
Matches	61;	Conservative 0;	Mismatches 32;	Indels 0; Gaps 0;

QY	25	TCGGTCTTCTTTACGGCTCAAGCCTGCTCTCAAGGCTCGACAGCTGTGGCCGCTGGC	84
Db	425	TCCGACTTCTCTGTCGAGAAAGTGTGCTCAGTTGCTCGACACGCTTGGCGGCTGGC	365
QY	85	GGGTCCGGCCGGCGCGGGGGCCGACACTGT	117
Db	365	GAGCAGGCTCGGGCTTTGGGCGCGCGCACTCT	333

[illegible]

TITLE	JOURNAL	COMMENT
USDA-WashU Neospora EST Project Unpublished (2000) Contact: Sandy Clifton, Ph.D. - Neospora USDA-WashU Neospora EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Contact David Sibley (toxest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.		

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Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .565
/organism="Neospora caninum"
/mol_type="mRNA"
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/lab_host="GC10 Competent Cells(PGC)"
/clone_lib="Nc-1 Tachyzoite cDNA Library 2"
/vector="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI: The cDNA library was constructed by Keliang Tang,
and Robert Cole at Washington University. cDNA was
synthesised from poly mRNA using an oligo-dT primer
containing a XhoI site. Following second strand synthesis,
EcoRI adapters were ligated to the cDNA, and products were
size-selected on sephacryl S500. The cDNA were
directionally cloned into the EcoRI/XhoI prepared
pBluescript II SK+ vector, and electroporated into GC10
Competent Cells(PGC). The library may contain a small
percentage of host or bacterial contaminants."

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ORIGIN

[illegible]

RESULT 15	CF261081/c	LOCUS	598 bp	mRNA	linear	EST 11-AUG-2003
DEFINITION	NCES73C80a11.y3	NC-Liv Tachyzoite	CDNA	Library	Neospora caninum	
			CDNA 5'	mRNA sequence.		

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 CF261081
 CF261081.1
 GI:33588654
 EST.
 Neospora caninum
 Neospora caninum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Sarcocystidae; Neospora.
 1 (bases 1 to 598)
 Cole R., Fogarty, S., Tang, K., Howe, D.K., Sibley, L.D., Clifton, S.,

Marra, M., Hillier, L., Pope, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tsagareashvili, R., Fedele, M., Belaygorod, L., Franklin, C., Carr, L. M., Grow, A., Maguire, L., Wadkins, J., Richey, J., Waterston, R. and Wilson, R.

TITLE	USDA-WashU Neospora EST Project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Sandy Clifton, Ph.D. - Neospora USDA-WashU Neospora EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Contact David Sibley (toxoeat@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seq primer: T3.

FEATURES
source

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/organism="Neospora caninum"
/mol_type="mRNA"
/db_xref="taxon:29176"
/dev_stage="Tachyzoite"
/lab_host="Electron Blue cells (Stratagene)"
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/clone lib="NC-LIV Tachyzoite cDNA Library"
/note="Vector: pBluescript II SK+Vector type: plasmid;
Site 1: EcoRI; Site 2: XhoI; The cDNA library was
constructed by Keliang Tang, and Robert Cole at Washington
University. cDNA was synthesized from Poly(A)+ mRNA using
an oligo-d(T) primer containing a XhoI site. Following
second strand synthesis, EcoRI adapters were ligated to
the cDNA, and products were size-selected on sephacryl
S500. The cDNA were directionally cloned into the
EcoRI/XhoI prepared pBluescript II SK+ vector, and
electroporated into Electrogen Blue cells (Stratagene).
The library may contain a small percentage of host or
bacterial contaminants."

ORIGIN

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Best Local Similarity 65.6%; Pred. No. 2.9;
Matches 61; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 85 GGGTCGCGCGCGCGCGCGCGCGCGCGACCTGT 117
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 534 GAGGCAGGCTCGGCGTTGGGCGCGCGCGACTCT 502
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: August 16, 2005, 05:21:56
Job time : 3183 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2005, 11:33:31 ; Search time 121.831 Seconds
(without alignments)
2390.439 Million cell updates/sec

Title: US-10-717-282-2
Perfect score: 4013
Sequence: 1 MAPWLQCSVFVTVNACLG.....CKADLGCRSYTDELHAVAPL 753

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4013	100.0	753	5	ABB07626 Human cyt
2	4003	99.8	753	5	ABB07627 Human cyt
3	3925	97.8	739	5	ABB07628 Human cyt
4	3901	97.2	738	4	Aau09904 Human Int
5	3897	97.1	738	4	Aau09953 Human Int
6	3896	97.1	738	4	Aau09954 Human Int
7	3894	97.0	738	4	Aau09951 Human Int
8	3894	97.0	738	4	Aau09952 Human Int
9	3894	97.0	738	4	Aau09956 Human Int
10	3890	96.9	738	4	Aau09957 Human Int
11	3890	96.9	738	4	Aau09955 Human Int
12	3830.5	95.5	738	5	Aau11355 Human DNA
13	3708	92.4	728	7	ADB65245 Human pro
14	3703	92.3	728	4	Aau04958 Human Int
15	3703	92.3	728	6	ABU089705 Human Int
16	3703	92.3	728	6	ABU72600 Human IL-
17	3703	92.3	728	6	ADA43241 Human Int
18	3703	92.3	728	7	ADA49782 Human Int
19	3703	92.3	728	7	ADA26975 Human PRO
20	3703	92.3	728	7	ADB66909 Human PRO
21	3703	92.3	728	7	ABW02061 Human IL-
22	3703	92.3	728	7	ADG87393 Human PRO
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24	3703	92.3	728	8	ADL16650 Human PRO
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ALIGNMENTS

RESULT 1

ABB07626
ID ABB07626 standard; protein; 753 AA.

AC ABB07626;

XX 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 amino acid sequence.

XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Preenell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX N-PSDB; ABA95031, ABA95032.

XX New cytokine receptor polypeptide designated zcytor18, useful for
inhibiting cell proliferation associated with psoriasis or tumor growth,
and modulating immune system by binding to endogenous zcytor18 ligand.

XX Claim 1; Page 2; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide
designated Zcytor18. The Zcytor18 polypeptides can be expressed by
standard recombinant methodology. The polypeptides can be used to inhibit
cell proliferation associated with psoriasis or tumour growth. The
encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
therapy techniques. Zcytor18 oligonucleotide probes are useful for in
vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
and localize Zcytor18 gene expression in tissue samples. The probes are
also useful for detecting gross aberrations in chromosome 3 in which
Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
linkage-based testing of pulmonary alveolar proteinosis, familial

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31	2699.5	67.3	554	5	AAU91330	AAU91330 Human nov
32	1337	33.3	296	4	AAU10601	AAU10601 5' portio
33	312	7.8	866	2	AAW04185	AAW04185 Human int
34	312	7.8	866	2	AAW61272	AAW61272 Human int
35	312	7.8	866	2	AAW92409	AAW92409 Human IL-
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37	312	7.8	866	3	AAW97181	AAW97181 Human int
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44	312	7.8	866	8	ADJ88265	ADJ88265 Human IL-
45	312	7.8	866	8	ADL24269	ADL24269 Human IL-

CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 amino acid sequence
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SQ Sequence 753 AA;
Query Match 100.0%; Score 4013; DB 5; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 721 PPALPSKLLSSGSKADLGCRSYTDDELHAVAPL 753
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XX ABB07627 standard; protein; 753 AA.
XX ABB07627;
XX
XX 20-MAY-2002 (first entry)
XX Human cytokine receptor, Zcytor18 variant sequence.
DE
XX

KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 269 /label= T269M
FT /note= "wild-type Thr is replaced with Met"
FT Misc-difference 750 /label= V750A
FT /note= "wild-type Val is replaced with Ala"
XX
XX W0200208259-A2.
XX
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-US0233253.
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Kuestner RE, Gao Z;
XX
XX WPI; 2002-217048/27.
DR N-PSDB; ABA95033, ABA95034.
XX
XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
XX
XX Disclosure; Page 94-98; 119pp; English.
XX
XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumour growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial
XX periodic fever and erythroleukemia, and erythroleukemia associated with
XX polymorphisms of cytokine receptors. The present sequence represents a
XX human Zcytor18 variant amino acid sequence
SQ Sequence 753 AA;
Query Match 99.8%; Score 4003; DB 5; Length 753;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 MAPWLQCSVFFTVNACLSQSLAAGGSGRARGADTCGRMKAAARPRLCVANEGVGP 60
Qy 61 ASRNSGLYNITFKYDNCCTTYLNPVKGKVIADAQNITISQYACHDOVAVTILWSPGALGIE 120
Db 61 ASRNSGLYNITFKYDNCCTTYLNPVKGKVIADAQNITISQYACHDOVAVTILWSPGALGIE 120
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Db 121 FLKGRFVILELXSEGRQCQQLILKDPKQLNSSFKRTGMESQPFNNMKFETDYFKVVVPF 180
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Db 541 QGSRNRYFRSKGRSLYVAICNMQHFIIDEEPDMFEKQFVPHPPPLRYREPVLKFDGSL 600
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQDGEARPALDGSAAALQPL 660
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Db 661 LHTVKGSPSPMDPRDSGIYDSSVPSSELSLPLMEGLSTDQTTSTSLTESVSSSGLGEE 720
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RESULT 3
ABB07628 standard; protein; 739 AA.
XX ABB07628;
AC ABB07628;
DT 20-MAY-2002 (first entry)
XX Human cytokine receptor, Zcytor18 splice variant.
DE Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;
KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
XX Homo sapiens.
OS WO200208259-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-US023253.
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Kuestner RE, Gao Z;
PI WPI; 2002-217048/27.
XX DR N-PSDB; ABA95035, ABA95036.
XX New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX Claim 1; Page 102-106; 119pp; English.

CC The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 splice variant
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SQ Sequence 739 AA;
Query Match 97.8%; Score 3925; DB 5; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
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Db 1 MAPWLQCSVFFTVNACLSQSLAAAGGSGRARGADTCGRMKAAARPLCLVANEGYGP 60
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Db 47 ASRNSGLYNTFFKYDNCCTTYLNPVGHVIAADAQNTISQYACHQDVAVTILWSPGALGIE 106
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Db 107 FLKGFVILBELKSEGRQCOQLIKDPKQLNSSFKRTGMESQPLNMKFETDYFVKVVPF 166
Qy 181 PSIKNESNYHPFFRTRACDILLQPDNLACPKFWKPRNLNISQSGDMQVDFDHPHNF 240
Db 167 PSIKNESNYHPFFRTRACDILLQPDNLACPKFWKPRNLNISQSGDMQVDFDHPHNF 226
Qy 241 PRFFYLKHEGPFRRKTKCQBOTTEMSTCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
Db 227 PRFFYLKHEGPFRRKTKCQBOTTEMSTCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286
Qy 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 360
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Qy 661 LHTVKGSPSPMDPRDSGIYDSSVPSSELSLPLMEGLSTDQTTSTSLTESVSSSGLGEE 720
Db 647 LHTVKGSPSPMDPRDSGIYDSSVPSSELSLPLMEGLSTDQTTSTSLTESVSSSGLGEE 706
Qy 721 PPALPSKLLSSGCKADIGCRSYTDELHAAVAPL 753
Db 707 PPALPSKLLSSGCKADIGCRSYTDELHAAVAPL 739

KW	hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW	bone disease; vascular disorder; eye disorder; cancer; mutant;
KW	mucin.
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 363
FT	/label= Ser, Thr, Ala, Cys
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XX	WO200168859-A2.
PX	20-SEP-2001.
PD	
XX	15-MAR-2001; 2001WO-US008678.
XX	
PF	16-MAR-2000; 2000US-0189816P.
XX	
PR	28-NOV-2000; 2000US-00724460.
XX	(AMGE-) AMGEN INC.
PA	
XX	Jing S;
PI	
DR	WPI; 2001-611392/70.
XX	
PT	Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT	for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT	psoriasis and glaucoma.
XX	
PS	Claim 20; Page; 158pp; English.
XX	
CC	The invention describes novel nucleic acids encoding interleukin (IL) 17
CC	receptor like polypeptides useful as vaccines and in gene therapy. These
CC	have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC	immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC	anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC	osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
CC	ophthalmological activities. The IL-17 receptor like nucleic acids and
CC	proteins may be used to prevent and treat diseases associated with
CC	inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
CC	include, for example immune disorders (e.g. inflammation, diabetes and
CC	transplant rejection), infections (e.g. hepatitis and septicemia),
CC	weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC	dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC	lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC	(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC	bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC	(e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
CC	breast cancer), reproductive disorders (e.g. infertility and
CC	miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC	DNA and its complements may also be used as diagnostic probes to detect and
CC	quantitate the presence of similar nucleic acids in samples and identify
CC	patients needing restorative therapy. The IL17rp may also be used as
CC	antigens in the production of antibodies against the proteins and in
CC	assays to identify modulators of expression and activity. The anti-
CC	IL17rp antibodies and antagonists may also be used to down regulate
CC	expression and activity. Note: This sequence is not given in the
CC	specification but is based on the human Interleukin 17 (IL-17) receptor
CC	like protein sequence (AAU09904) and has been created according to
CC	information given in claim 20
XX	
XX	Sequence 738 AA;
XX	
Query Match	97.1%; Score 3897; DB 4; Length 738;
Best Local Similarity	97.5%; Pred. No. 0;
Matches 733; Conservative	1; Mismatches 4; Indels 14; Gaps 1;
QY	1 MAPWLQLCSVFVTNACLSGSLAVALAGSGRGARGADTCGRWKAAAPRLCVANEGVGP 60
DB	1 MAPWLQLCSVFVTNACLSGSLAVALAGSGRGANGVDTCGR-----GVGP 46
QY	61 ASRNSGLYNITFKYDNCITYLNPVGKHIADAQNITISQYACHDQAVNTILMSPGALGIE 120

(AMGE-) AMGEN INC.
 Jing S;
 WPI; 2001-611392/70.
 Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
 Claim 18; Page; 159pp; English.
 The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09952) and has been created according to information given in claim 18
 Sequence 738 AA;
 Query Match 97.0%; Score 3894; DB 4; Length 738;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;
 QY 1 MAPWLQCSVFTVFNACLSQSLAAGSGRGARGADTCGWRMKAARPRLCVANEVGP 60
 DB 1 MAPWLQCSVFTVFNACLSQSLAAGSGRGARGADTCGWRMKAARPRLCVANEVGP 46
 QY 61 ASRNSGLYNITPKYDNCITLYNPVKHVIADAQNTISQYACHDQVAVTILWSPGALGIE 120
 DB 47 ASRNSGLYNITPKYDNCITLYNPVKHVIADAQNTISQYACHDQVAVTILWSPGALGIE 106
 QY 121 FLKGRVILELKSGRGCOQLIKDPKQLNSFKRTGMSOPFLNMFETDYFKVVPF 180
 DB 107 FLKGRVILELKSGRGCOQLIKDPKQLNSFKRTGMSOPFLNMFETDYFKVVPF 166
 QY 181 PSIKNESYHPFFETTRACDILLOPNLACKPFWKPRNLNLSQHGSDMQVSDHAPHNFG 240
 DB 167 PSIKNESYHPFFETTRACDILLOPNLACKPFWKPRNLNLSQHGSDMQVSDHAPHNFG 226
 QY 241 PRFFYLHYLKHGPFKRTKQEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
 DB 227 PRFFYLHYLKHGPFKRTKQEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286
 QY 301 LKPVHSPWAGPIRAVAVTIVPLVVISAFATLFTVMCKKQEQNIYSHLDESESESTYTA 360
 DB 287 LKPVHSPWAGPIRAVAVTIVPLVVISAFATLFTVMCKKQEQNIYSHLDESESESTYTA 346
 QY 361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420

PA DB 347 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406
 XX QY 421 WVIQKHESQFIIVVCSKGMKYFVDKKNYKHGGSGSGKGFPLVAVSAIAEKLRAQK 480
 XX DB 407 WVIQKHESQFIIVVCSKGMKYFVDKKNYKHGGSGSGKGFPLVAVSAIAEKLRAQK 466
 XX QY 481 SSSAALSFKTAVFYDSCGDPGILDLSTKYRLMDNLPOLCSHLHSDHGLQBPQGHTR 540
 XX DB 467 SSSAALSFKTAVFYDSCGDPGILDLSTKYRLMDNLPOLCSHLHSDHGLQBPQGHTR 526
 XX QY 541 QGSRNRYFRKSGSLYVAICNMHOFIDEBPDWFEKQFVFPHPPLRYREPVLKFDGSL 600
 XX DB 527 QGSRNRYFRKSGSLYVAICNMHOFIDEBPDWFEKQFVFPHPPLRYREPVLKFDGSL 586
 XX QY 601 VLNDVMCKPESDFCLKVEAAVLGATGPADSDSHQSGHGGIDQDGEARPALDGSAAQLPL 660
 XX DB 587 VLNDVMCKPESDFCLKVEAPVLGATGPADSDSHQSGHGGIDQDGEARPALDGSAAQLPL 646
 XX QY 661 LHTVKAGSPDMPRDSGIDYSSVPSSELSPLMEGLSTDQTTSTSLTESVSSSGLGBEE 720
 XX DB 647 LHTVKAGSPDMPRDSGIDYSSVPSSELSPLMEGLSTDQTTSTSLTESVSSSGLGBEE 706
 QY 721 PPALPSKLLSSGCKADLGRSYTDELHAVAP 752
 DB 707 PPALPSKLLSSGCKADLGRSYTDELHAVAP 738
 RESULT 8
 AAU09952
 ID AAU09952 standard; protein; 738 AA.
 XX AC AAU09952;
 XX AC AAU09952;
 DT 14-FEB-2002 (first entry)
 XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #2.
 XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mitein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 227 /label= Phe, Leu, Val, Ile, Ala, Tyr
 XX PN WO200168859-A2.
 XX PD 20-SEP-2001.
 XX PF 15-MAR-2001; 2001WO-US0008678.
 XX PR 16-MAR-2000; 2000US-0189816P.
 XX PR 28-NOV-2000; 2000US-00724460.
 XX PA (AMGE-) AMGEN INC.
 XX PI Jing S;
 XX WI WPI; 2001-611392/70.
 XX PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.

PS Claim 19; Page; 158pp; English.

CC The invention describes novel nucleic acids encoding interleukin (IL) 17

CC receptor like polypeptides useful as vaccines and in gene therapy. These

CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,

CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,

CC anti-parkinsonian, anti-convulsant, anti-aesthetic, dermatological,

CC osteopathic, vascular, cycostatic, anti-leukaemic, anti-infertility and

CC ophthalmological activities. The IL-17 receptor like nucleic acids and

CC proteins may be used to prevent and treat diseases associated with

CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These

CC include, for example immune disorders (e.g. inflammation, diabetes and

CC transplant rejection), infections (e.g. hepatitis and septicemia),

CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal

CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),

CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease

CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),

CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders

CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and

CC breast cancer), reproductive disorders (e.g. infertility and

CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The

CC DNA and its complements may also be used as diagnostic probes to detect and

CC quantitate the presence of similar nucleic acids in samples and identify

CC patients needing restorative therapy. The IL17rlp may also be used as

CC antigens in the production of antibodies against the proteins and in

CC assays to identify modulators of expression and activity. The anti-

CC IL17rlp antibodies and antagonists may also be used to down regulate

CC expression and activity. Note: This sequence is not given in the

CC specification but is based on the human Interleukin 17 (IL-17) receptor

CC like protein sequence (AAU09904) and has been created according to

CC information given in claim 19

XX Sequence 738 AA;

SQ

Query Match 97.0%; Score 3894; DB 4; Length 738;

Best Local Similarity 97.5%; Pred. No. 0;

Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFTVNAACINGSQAVAGGSGRARGADTCGRMKAAARPLCVANEGVGP 60

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1 MAPWLQCSVFTVNAACINGSQAVAGGSGRARGADTCGRMKAAARPLCVANEGVGP 46

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 ASRNSGLVNTIFKDYNDCTTLYNPVGHVIAQAQNTISQVACHDOVATILWSPGALGIE 120

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 47 ASRNSGLVNTIFKDYNDCTTLYNPVGHVIAQAQNTISQVACHDOVATILWSPGALGIE 106

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 FLKGFVILELSEKSGRQCQQLILKDPKQLNSSFRTGMSQPFLLNMFETDYFKVVPVF 180

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 107 FLKGFVILELSEKSGRQCQQLILKDPKQLNSSFRTGMSQPFLLNMFETDYFKVVPVF 166

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 PSIKNESNYHPFRTTRACDILLQPDNLACKFPFWKPRNLNISQHGSDMQVSYFDHAPNFG 240

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 167 PSIKNESNYHPFRTTRACDILLQPDNLACKFPFWKPRNLNISQHGSDMQVSYFDHAPNFG 226

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 241 PRFFYLHYLKHGEPFKRCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 227 XRFYLHYLKHGEPFKRCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 360

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 346

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 361 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 420

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 347 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 406

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 421 WVIQKHESQPIIVVCSKGMKYFYVDKKNYKHKGSGGSGKGLFLVAVSAEKLRAQK 480

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 407 WVIQKHESQPIIVVCSKGMKYFYVDKKNYKHKGSGGSGKGLFLVAVSAEKLRAQK 466

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 481 SSSAALSKFIIVVCSKGMKYFYVDKKNYKHKGSGGSGKGLFLVAVSAEKLRAQK 540

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 467 SSSAALSKFIIVVCSKGMKYFYVDKKNYKHKGSGGSGKGLFLVAVSAEKLRAQK 526

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 541 QGSRNRYFSKSGSLYVAICNMHQFIDEBPDWFEKQFVFPFPPPLRYRBPVLEKFDGSL 600

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 527 QGSRNRYFSKSGSLYVAICNMHQFIDEBPDWFEKQFVFPFPPPLRYRBPVLEKFDGSL 586

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSGHSGHGLDQDGEARPALDGSAAALQPL 660

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 587 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSGHSGHGLDQDGEARPALDGSAAALQPL 646

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 661 LHTVKGSPSDMPDRSGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSSSSSGLGEE 720

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 647 LHTVKGSPSDMPDRSGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSSSSSGLGEE 706

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 721 PPALPSKLLSSGSKADLGRSYTDELHAVAP 752

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 707 PPALPSKLLSSGSKADLGRSYTDELHAVAP 738

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9

AAU09956

ID AAU09956 standard; protein; 738 AA.

XX

AC AAU09956;

XX

DT 14-FEB-2002 (first entry)

XX

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.

XX

KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;

KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;

KW anti-convulsant; anti-aesthetic; dermatological; renal; osteopathic;

KW vascular; cycostatic; anti-leukaemic; anti-infertility; ophthalmological;

KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;

KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;

KW mtein.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX

FH Key Location/Qualifiers

FT Misc-difference 515

FT /label= Asp, Glu

FT

PN W0200168859-A2.

XX

PD 20-SEP-2001.

XX

XX

PF 15-MAR-2001; 2001WO-US008678.

XX

PR 16-MAR-2000; 2000US-0189816P.

PR 28-NOV-2000; 2000US-00724460.

XX

PA (AMGE-) AMGEN INC.

XX

PI Jing S;

XX

DR WPI; 2001-611392/70.

XX

XX

PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful

PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,

PT psoriasis and glaucoma.

XX

PS Claim 23; Page; 158pp; English.

XX

CC The invention describes novel nucleic acids encoding interleukin (IL) 17

CC receptor like polypeptides useful as vaccines and in gene therapy. These

CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,

CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,

CC anti-parkinsonian, anti-convulsant, anti-aesthetic, dermatological,

CC osteopathic, vascular, cycostatic, anti-leukaemic, anti-infertility and

CC ophthalmological activities. The IL-17 receptor like nucleic acids and

CC proteins may be used to prevent and treat diseases associated with

CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicemia),
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human Interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 23
XX
SQ Sequence 738 AA;

Query Match 97.0%; Score 3894; DB 4; Length 738;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFTVYACVAGGSGARAGADTCGRWMAAARPRCLVANEGVGP 60
Db 1 MAPWLQCSVFTVYACVAGGSGARAGADTCGRWMAAARPRCLVANEGVGP 60

Qy 61 ASRNSGLYNTIFKDYDNCNTYLNPNKGVIAQAQNTISQYACHDOVAATILWSPGALGIE 120
Db 47 ASRNSGLYNTIFKDYDNCNTYLNPNKGVIAQAQNTISQYACHDOVAATILWSPGALGIE 106

Qy 121 FLKGRVLTLEBKSGRQCQQLIKDPKQLNSSFKRTGMSQPFLLMKFFETDYFKVVPF 180
Db 107 FLKGRVLTLEBKSGRQCQQLIKDPKQLNSSFKRTGMSQPFLLMKFFETDYFKVVPF 166

Qy 181 PSIKNESNYHPFFRTRACDLLLLQDNLACKPFWKPRNLNISQHGSDMQVDFHAPNFG 240
Db 167 PSIKNESNYHPFFRTRACDLLLLQDNLACKPFWKPRNLNISQHGSDMQVDFHAPNFG 226

Qy 241 FRPFYLYLKHGEGPKRKTCKQEQTTTSCLLQNVSPGDIYIELVDVDTNTTKVWHYA 300
Db 227 FRPFYLYLKHGEGPKRKTCKQEQTTTSCLLQNVSPGDIYIELVDVDTNTTKVWHYA 286

Qy 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346

Qy 361 LPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 406

Qy 421 VWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRGSGKGEFLFVAVSAIAEKLRAQK 480
Db 407 VWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRGSGKGEFLFVAVSAIAEKLRAQK 466

Qy 481 SSSAALSXFIAVYPDYSCEGDPVGLDLSKYRLMDNLPQLCSHLHSDHGLQEPGQTR 540
Db 467 SSSAALSXFIAVYPDYSCEGDPVGLDLSKYRLMDNLPQLCSHLHSDHGLQEPGQTR 526

Qy 541 QGSRNRYFRSKSGRSLYVAICNMHQFIDEEPDPWFKEQFVPPHPPPLRYREPVLEKFDGSL 600
Db 527 QGSRNRYFRSKSGRSLYVAICNMHQFIDEEPDPWFKEQFVPPHPPPLRYREPVLEKFDGSL 586

Qy 601 VLNDVMCKPGPESDFCLKVEAVLGTATGPADSPQHSQHGGLDQDGEARPALDGSAAQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAVLGTATGPADSPQHSQHGGLDQDGEARPALDGSAAQPL 646

Qy 661 LHTVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTSSVSSSGLGEE 720

Db 647 LHTVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTSSVSSSGLGEE 706

Qy 721 PPALPSKLLSGGCKADLGRSYTDELHAVAP 752

Db 707 PPALPSKLLSGGCKADLGRSYTDELHAVAP 738

RESULT 10
AAU09957
ID AAU09957 standard; protein; 738 AA.
XX AC
XX AAU09957;
XX 14-FEB-2002 (first entry)
XX Human Interleukin 17 (hIL-17) receptor like protein substitution #7.
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutein.
XX Homo sapiens.
XX Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 602 /label= Cys, Ala, Ser
FT
XX WO200168959-A2.
XX 20-SEP-2001.
XX 15-MAR-2001; 2001WO-US008678.
XX 16-MAR-2000; 2000US-0189816P.
XX 28-NOV-2000; 2000US-00724460.
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
XX WPI; 2001-611392/70.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX
XX Claim 24; Page; 159pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and

CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human Interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 24
XX
SQ Sequence 738 AA;

Query Match 96.9%; Score 3890; DB 4; Length 738;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFTTNACLNGSOLAVAGGSGRARGADTCGRMKAAARPRCLCVANEGVGP 60
DB 1 MAPWLQCSVFTTNACLNGSOLAVAGGSGRANGVDTGWR-----GVGP 46

QY 61 ASRNSGLYNTFFKYDNCCTYLPVKGHVIADAQNITISQYACHDQVAVTILMSPGALGIE 120
DB 47 ASRNSGLYNTFFKYDNCCTYLPVKGHVIADAQNITISQYACHDQVAVTILMSPGALGIE 106

QY 121 FLKGFVILELKEGRCQCOOLILKDPKOLNSSFKRTGMSOPFLNKKFTDYVKKVVPF 180
DB 107 FLKGFVILELKEGRCQCOOLILKDPKOLNSSFKRTGMSOPFLNKKFTDYVKKVVPF 166

QY 181 PSIKNESNYHFFPFRTRACDLLLPDNLACKPFWKPRNLNISQHGSDMQVSFHDHAPNFG 240
DB 167 PSIKNESNYHFFPFRTRACDLLLPDNLACKPFWKPRNLNISQHGSDMQVSFHDHAPNFG 226

QY 241 FRPFYLHYKLKHEGPFKRTCKQBTQTTTSCLLQNVSPGDYIIELVDDNTNTRKVMHYA 300
DB 227 FRPFYLHYKLKHEGPFKRTCKQBTQTTTSCLLQNVSPGDYIIELVDDNTNTRKVMHYA 286

QY 301 LKPVHSPWAGIRAVATVPLVAVISAFATLFTVWCRKKQENIYSHLDESSSSTYTAA 360
DB 287 LKPVHSPWAGIRAVATVPLVAVISAFATLFTVWCRKKQENIYSHLDESSSSTYTAA 346

QY 361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQFCGCEVALDLWEDFSLCREGORE 420
DB 347 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQFCGCEVALDLWEDFSLCREGORE 406

QY 421 WVIQKIHESQPIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRQAKQ 480
DB 407 WVIQKIHESQPIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRQAKQ 466

QY 481 SSSAALSXFIAVFDYSCGEGVPGILDLSTKYRLMDNLPQLCSHLHRDHGLQEPGQHTR 540
DB 467 SSSAALSXFIAVFDYSCGEGVPGILDLSTKYRLMDNLPQLCSHLHRDHGLQEPGQHTR 526

QY 541 QGSRNRTFRSKGSLVVAICNMHQFIDEEPDPWEKQFVPPHPPLYRREPLVKFPDGL 600
DB 527 QGSRNRTFRSKGSLVVAICNMHQFIDEEPDPWEKQFVPPHPPLYRREPLVKFPDGL 586

QY 601 VLNDVMCKPGPESDFCLKVEAVLIGATGPADSQHSQHGLDQDGEARPALDGSAAQLQPL 660
DB 587 VLNDVMCKPGPESDFCLKVEAVLIGATGPADSQHSQHGLDQDGEARPALDGSAAQLQPL 646

QY 661 LHTVKAQSPMPDRSDGIDYSSVPSSELSLPLMEGLSTDQTTSTSLTESVSSSGLGEE 720
DB 647 LHTVKAQSPMPDRSDGIDYSSVPSSELSLPLMEGLSTDQTTSTSLTESVSSSGLGEE 706

QY 721 PPALPSKLLSGSGCKADLCGRSYTDELHAVAP 752
DB 707 PPALPSKLLSGSGCKADLCGRSYTDELHAVAP 738

ID AAU09955 standard; protein; 738 AA.
XX
AC AAU09955;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mucin.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 385 /label= Cys, Ser, Ala
XX FT
XX PN WO200168859-A2.
XX
XX PD 20-SEP-2001.
XX
XX PF 15-MAR-2001; 2001WO-US0008678.
XX
XX PR 16-MAR-2000; 2000US-0189816P.
XX PR 28-NOV-2000; 2000US-00724460.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Jing S;
XX PI WPI; 2001-611392/70.
XX
XX PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX
XX PS Claim 22; Page; 158pp; English.
XX
XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-leukaemic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rlp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The anti-
XX IL17rlp antibodies and antagonists may also be used to down regulate
XX expression and activity. Note: This sequence is not given in the
XX specification but is based on the human Interleukin 17 (IL-17) receptor
XX like protein sequence (AAU09904) and has been created according to


```
CC information given in claim 22
XX Sequence 738 AA;
SQ Query Match 96.9%; Score 3890; DB 4; Length 738;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFVTNACLSQSLAVAGGSGRARGADTCGWRMKAARPRLCVANEGVGP 60
DB 1 MAPWLQCSVFVTNACLSQSLAVAGGSGRARGADTCGWRMKAARPRLCVANEGVGP 46

QY 61 ASRNSGLYNIITFKYDNCCTTYLNPVKGKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 120
DB 47 ASRNSGLYNIITFKYDNCCTTYLNPVKGKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 106

QY 121 FLKGFVRVILEELKSEGROCCQLILKDPKQLNSSFRTGMSQPFLLNMFETDVFYKVPVF 180
DB 107 FLKGFVRVILEELKSEGROCCQLILKDPKQLNSSFRTGMSQPFLLNMFETDVFYKVPVF 166

QY 181 PSIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISOHGSMDQVSPDHAPHNFG 240
DB 167 PSIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISOHGSMDQVSPDHAPHNFG 226

QY 241 FRFFYLHYKLKHGEPFKRKTCKEQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
DB 227 FRFFYLHYKLKHGEPFKRKTCKEQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286

QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 360
DB 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346

QY 361 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAYFLQDFXGCEVALDLWEDFSLCREGORE 420
DB 347 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAYFLQDFXGCEVALDLWEDFSLCREGORE 406

QY 421 WVIQIHESQFIIVVCSGKMYFVDKKNYKHGGRSGKGEFLFVAVSAIAEKLRQAKQ 480
DB 407 WVIQIHESQFIIVVCSGKMYFVDKKNYKHGGRSGKGEFLFVAVSAIAEKLRQAKQ 466

QY 481 SSSAALSXFIAYFDYSCGDPVPGILDSTKYRLMDNLPLQCSHLHSDHGLQBPQHTR 540
DB 467 SSSAALSXFIAYFDYSCGDPVPGILDSTKYRLMDNLPLQCSHLHSDHGLQBPQHTR 526

QY 541 QGSRNRYPRSGRSLYVAICNMHQFIDEEPDWFQKQVPPHPPRLRYREPVELEKFDGSL 600
DB 527 QGSRNRYPRSGRSLYVAICNMHQFIDEEPDWFQKQVPPHPPRLRYREPVELEKFDGSL 586

QY 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQDGEARPALDGSAAQLPL 660
DB 587 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSQHSQHGGLDQDGEARPALDGSAAQLPL 646

QY 661 LHTVAGSPSPDRSDGIVSDSPSSLSPLMEGLSTDTQETSSLTSSVSSSSGLGEE 720
DB 647 LHTVAGSPSPDRSDGIVSDSPSSLSPLMEGLSTDTQETSSLTSSVSSSSGLGEE 706

QY 721 PPALPSKLLSSGCKADLCGRSYTDELHNAVAP 752
DB 707 PPALPSKLLSSGCKADLCGRSYTDELHNAVAP 738

RESULT 12
AAU11355
XX AAU11355 standard; protein; 738 AA.
XX AC AAU11355;
XX DT 26-MAR-2002 (first entry)
XX DE Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.
XX KW Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;
KW gene therapy; protein therapy; immunological disorder.
```

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XX Homo sapiens.
XX OS
XX FH Key Location/Qualifiers
XX FT Misc-difference 25 /label= Val
XX FT FT /note= "Encoded by GTN"
XX
XX FN WO200190358-A2.
XX PD 29-NOV-2001.
XX
XX PF 23-MAY-2001; 2001WO-US016767.
XX PR 24-MAY-2000; 2000US-0206862P.
XX
XX PA (SCHE ) SCHERING CORP.
XX PI Gorman DM;
XX
XX DR WPI; 2002-106198/14.
XX
XX PT N-PSDB; AAS18134.
XX
XX PT Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
XX PT useful for detecting antibodies generated in response to presence of
XX PT increased protein levels or immunological disorders.
XX
XX PS Claim 1; Page 25; 148pp; English.
XX
XX CC The invention relates to primate and rodent DNAX cytokine receptor
XX CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
XX CC receptors, or their portions may be useful as phosphate labelling enzymes
XX CC to label general or specific substrates. The subunits may also be
XX CC functional immunogens to elicit recognising antibodies, or antigens
XX CC capable of binding antibodies. A combination, e.g., including a DCRS can
XX CC be used as an immunogen for the production of antisera or antibodies
XX CC capable of distinguishing between other cytokine receptor family members.
XX CC A purified DCRS can also be used as a reagent to detect antibodies
XX CC generated in response to the presence of elevated levels of expression,
XX CC or immunological disorders which lead to antibody production to the
XX CC endogenous receptor. This sequence represents the human DCRS8 polypeptide
XX
XX SQ Sequence 738 AA;
Query Match 95.5%; Score 3830.5; DB 5; Length 738;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 725; Conservative 2; Mismatches 11; Indels 15; Gaps 2;

QY 1 MAPWLQCSVFVTNACLSQSLAVAGGSGRARGADTCGWRMKAARPRLCVANEGVGP 60
DB 1 MAPWLQCSVFVTNACLSQSLAVAGGSGRARGADTCGWRMKAARPRLCVANEGVGP 46

QY 61 ASRNSGLYNIITFKYDNCCTTYLNPVKGKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 120
DB 47 ASRNSGLYNIITFKYDNCCTTYLNPVKGKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 106

QY 121 FLKGFVRVILEELKSEGROCCQLILKDPKQLNSSFRTGMSQPFLLNMFETDVFYKVPVF 180
DB 107 FLKGFVRVILEELKSEGROCCQLILKDPKQLNSSFRTGMSQPFLLNMFETDVFYKVPVF 165

QY 181 PSIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISOHGSMDQVSPDHAPHNFG 240
DB 166 PSIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISOHGSMDQVSPDHAPHNFG 225

QY 241 FRFFYLHYKLKHGEPFKRKTCKEQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
DB 226 FRFFYLHYKLKHGEPFKRKTCKEQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 285

QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 360
DB 286 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 345

QY 361 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAYFLQDFXGCEVALDLWEDFSLCREGORE 420
```


|||||
Db 346 LPRERLRPRKVFVLCYSSKQGNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCREQRE 405
Qy 421 WVIQKHESQPIIVVCSKGMKYFVDKKNYKHKGGRSGKGLFLVAVSAIAEKLROAKQ 480
Db 406 WVIQKHESQPIIVVCSKGMKYFVDKKNYKHKGGRSGKGLFLVAVSAIAEKLROAKQ 465
Qy 481 SSSAALSFTAVFDYCEGDVPGILDSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 540
Db 466 SSSAALSFTAVFDYCEGDVPGILDSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 525
Qy 541 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQFVPPHPPPLRYRPPVLEKFDPSGL 600
Db 526 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQFVPPHPPPLRYRPPVLEKFDPSGL 585
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGIDQDGEARPALDGSAAQPL 660
Db 586 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGIDQDGEARPALDGSAAQPL 645
Qy 661 LHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSSSSGLGEEE 720
Db 646 LHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSSSSGLGEEE 705
Qy 721 PPALPSKLLSGSGCKADLGCRSYTDLHVAAPL 753
Db 706 PPALPSKLLSGSGCKADLGCRSYTDLHVAAPL 738
RESULT 13
ADB65245
ID ADB65245 standard; protein; 728 AA.
XX
AC ADB65245;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human protein encoded by clone TESTI20046540.
XX
KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
cell regeneration; membrane protein; signal transduction-related protein;
transcription-related protein; osteoporosis; neurological disease;
cancer; tumour.
XX
OS Homo sapiens.
XX
PN EP1308459-A2.
XX
PD 07-MAY-2003.
XX
PF 28-MAR-2002; 2002EP-00007401.
XX
PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR N-PSDB; ADB63275.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide

or its partial peptide, an antibody binding to the polypeptide or peptide
of the polynucleotide, immunologically assaying the polypeptide or
peptide of the polynucleotide by contacting the polypeptide or peptide
with the antibody of the encoded protein, and observing the binding
between the two, a transformant carrying the polynucleotide in an
expressible manner and an antisense polynucleotide. The oligonucleotide
is useful as a primer for synthesising the polynucleotide, or as a probe
for detecting the polynucleotide. The polynucleotides and encoded
proteins are useful as pharmaceutical agents and many disease-related
genes may be included in them, for developing a diagnostic marker or
medicines for regulation of their expression and activity, or as targets
of gene therapy. The genes are involved in tissue and/or cell
regeneration. Membrane proteins, signal transduction-related proteins,
transcription-related proteins, disease-related proteins and genes
encoding them can be used as indicators for diseases (e.g. osteoporosis,
neurological diseases, cancer, tumours. The cDNA may be used to regulate
the activity or expression of the encoded protein to treat diseases. The
sequence presented is a protein of the invention. Note: Some of the
sequence data for this patent is not represented in the printed
specification, but is based on sequence information supplied by the
European Patent Office.
XX
SQ Sequence 728 AA;
Query Match 92.4%; Score 3708; DB 7; Length 728;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 56 EGVGPASRNSGLYNITFKYDNCCTTYLNPVGHVIAQAQNTITISQYACHQDVAVTILMSPG 115
Db 31 QGVGPASRNSGLYNITFKYDNCCTTYLNPVGHVIAQAQNTITISQYACHQDVAVTILMSPG 90
Qy 116 ALGIEFLKGRFVILEELKSGROCOQLILKDPQLNSSFKRTGMESQFPLNMKPTDYFV 175
Db 91 ALGIEFLKGRFVILEELKSGROCOQLILKDPQLNSSFKRTGMESQFPLNMKPTDYFV 150
Qy 176 KVVPPFSIKNESNVHPFFRTRACDILLQPDNLACKPFWKPRNLINISQHSQDMQVSPDHA 235
Db 151 KVVPPFSIKNESNVHPFFRTRACDILLQPDNLACKPFWKPRNLINISQHSQDMQVSPDHA 210
Qy 236 PHNFGFRFFYLHYKLKHEGPFKRTCKEQTTTSCLLQNVSPGDYIILVDDTNTTRK 295
Db 211 PHNFGFRFFYLHYKLKHEGPFKRTCKEQTTTSCLLQNVSPGDYIILVDDTNTTRK 270
Qy 296 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKQOENIYSHLDESSSS 355
Db 271 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKQOENIYSHLDESSSS 330
Qy 356 TYTAALPRERLRPRKVFVLCYSSKQGNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCR 415
Db 331 TYTAALPRERLRPRKVFVLCYSSKQGNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCR 390
Qy 416 EGQREWVIQKHESQPIIVVCSKGMKYFVDKKNYKHKGGRSGKGLFLVAVSAIAEKL 475
Db 391 EGQREWVIQKHESQPIIVVCSKGMKYFVDKKNYKHKGGRSGKGLFLVAVSAIAEKL 450
Qy 476 ROAKQSSAALSFTAVFDYCEGDVPGILDSTKYRLMDNLPLQCSHLHSDHGLQEP 535
Db 451 ROAKQSSAALSFTAVFDYCEGDVPGILDSTKYRLMDNLPLQCSHLHSDHGLQEP 510
Qy 536 GQHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQFVPPHPPPLRYRPPVLEK 595
Db 511 GQHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQFVPPHPPPLRYRPPVLEK 570
Qy 596 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGIDQDGEARPALDGS 655
Db 571 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGIDQDGEARPALDGS 630
Qy 656 ALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSSSS 715
Db 631 ALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSSSS 690
Qy 716 LGBEEPPALPSKLLSGSGCKADLGCRSYTDLHVAAPL 753

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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:38:07 ; Search time 30.7138 Seconds
(without alignments)
1830.146 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3703	92.3	728	4	US-09-747-259-18 Sequence 18, Appl
2	3703	92.3	728	4	US-09-816-744-18 Sequence 18, Appl
3	312	7.8	866	2	US-08-620-694A-10 Sequence 10, Appl
4	312	7.8	866	3	US-09-022-255-10 Sequence 10, Appl
5	312	7.8	866	3	US-09-022-696-10 Sequence 10, Appl
6	312	7.8	866	3	US-08-978-773-4 Sequence 4, Appl
7	312	7.8	866	3	US-09-022-253-10 Sequence 10, Appl
8	312	7.8	866	3	US-09-022-260-10 Sequence 10, Appl
9	312	7.8	866	3	US-09-022-259-10 Sequence 10, Appl
10	312	7.8	866	3	US-09-022-257-10 Sequence 10, Appl
11	312	7.8	866	4	US-09-549-679-10 Sequence 10, Appl
12	312	7.8	866	4	US-10-033-522-1 Sequence 1, Appl
13	306	7.6	864	2	US-08-620-694A-2 Sequence 2, Appl
14	306	7.6	864	3	US-09-022-255-2 Sequence 2, Appl
15	306	7.6	864	3	US-09-022-696-2 Sequence 2, Appl
16	306	7.6	864	3	US-08-978-773-2 Sequence 2, Appl
17	306	7.6	864	3	US-09-022-253-2 Sequence 2, Appl
18	306	7.6	864	3	US-09-022-260-2 Sequence 2, Appl
19	306	7.6	864	3	US-09-022-259-2 Sequence 2, Appl
20	306	7.6	864	3	US-09-022-257-2 Sequence 2, Appl
21	306	7.6	864	4	US-09-549-679-2 Sequence 106, App
22	135.5	3.4	385	4	US-09-593-360B-106 Sequence 12, Appl
23	135.5	3.4	502	4	US-09-747-259-12 Sequence 12, Appl
24	135.5	3.4	502	4	US-09-816-744-12 Sequence 11658, A
25	135.5	3.4	504	4	US-09-949-016-11658 Sequence 1, Appl
26	116.5	2.9	993	1	US-08-348-143-1 Sequence 1, Appl
27	116.5	2.9	993	1	US-08-571-785-1 Sequence 1, Appl

Sequence 1, Appli
Sequence 1, Appli
Sequence 8005, Ap
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 303, App
Sequence 303, App
Sequence 6384, Ap
Sequence 25826, A
Sequence 9916, Ap
Sequence 9917, Ap
Sequence 10562, A
Sequence 14749, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 664, App
Sequence 6898, Ap

ALIGNMENTS

RESULT 1

US-09-747-259-18

; Sequence 18, Application US/09747259

; Patent No. 6569645

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Hanzhong

; APPLICANT: Hillan, Kenneth

; APPLICANT: Tumas, Daniel

; APPLICANT: VanLookeren, Menno

; APPLICANT: Vandlen, Richard

; APPLICANT: Watanabe, Colin

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C1P1(US)

; CURRENT APPLICATION NUMBER: US/09/747,259

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: US 09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/172,096

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: PCT/US99/31274

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: US 60/175,481

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: PCT/US00/04341

; PRIOR FILING DATE: 2000-02-18

; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 60/191,007

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: PCT/US00/07532

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: PCT/US00/15264

; PRIOR FILING DATE: 2000-06-02

; PRIOR APPLICATION NUMBER: US 60/213,087

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: US 09/644,848

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

;; PRIOR APPLICATION NUMBER: US 60/242,837
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: US 60/253,646
;; PRIOR FILING DATE: 2000-11-28
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 18
;; LENGTH: 728
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-747-259-18

Query Match 92.3%; Score 3703; DB 4; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;
QY 42 RMKAARPRLCVANE-GVGPSARNISGLYNTTFKYDNCCTTYLNPVKGHVIAADAQNITISQY 100
DB 3 RASASGVPALFVSGEQGVGPASRNSGLYNTTFKYDNCCTTYLNPVKGHVIAADAQNITISQY 62
QY 101 ACHDQAVATILWSFGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSSFPKRTGME 160
DB 63 ACHDQAVATILWSFGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSSFPKRTGME 122
QY 161 SQPLNNKFTDYFVKVVPFPPSIKNESNYHPFPRTRACDILLQPDNLACKPFWKPRNLN 220
DB 123 SQPLNNKFTDYFVKVVPFPPSIKNESNYHPFPRTRACDILLQPDNLACKPFWKPRNLN 182
QY 221 ISQ-----HGSDMQVSFDHAPHNFGFRFFVLYHKLKHEGPFKRKTCQSQTT 267
DB 183 ISQHGSDMQVSFDHAPHNFGFRFFVLYHKLKHEGPFKRKTCQSQTT 242
QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302
QY 328 ATLFTVMCRKQKQENIYSHLDDESSSSTYTAALPRERLRPRPKVFLCYSSKQGNHNV 387
DB 303 ATLFTVMCRKQKQENIYSHLDDESSSSTYTAALPRERLRPRPKVFLCYSSKQGNHNV 362
QY 388 VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKK 447
DB 363 VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKK 422
QY 448 NYKHGGGRSGKGEFLVAVSAIAEKLRAQKQSSAALSFKFIAYVFDYSCGQVPGILD 507
DB 508 LSTKYRLMDNLPLQCSHLHSDHGLQBPQHTQGRSRNRYFRSKSGRSLYVAICNMHQFI 567
QY 483 LSTKYRLMDNLPLQCSHLHSDHGLQBPQHTQGRSRNRYFRSKSGRSLYVAICNMHQFI 542
QY 568 DEEDPWFKEQVFPFPPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 627
DB 543 DEEDPWFKEQVFPFPPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 602
QY 628 GPADSQHSQHGGLDQGEARPALDGSAAQLPLLHTVKAGSPSPMPDRSDGIYSSVPSSE 687
DB 603 GPADSQHSQHGGLDQGEARPALDGSAAQLPLLHTVKAGSPSPMPDRSDGIYSSVPSSE 662
QY 688 LSLPLMEGLSTDQETSLTESVSSSGLGEEPPALPSKLLSSGSKADLGCRSYTDEL 747
DB 663 LSLPLMEGLSTDQETSLTESVSSSGLGEEPPALPSKLLSSGSKADLGCRSYTDEL 722
QY 748 HAVAPL 753
DB 723 HAVAPL 728

RESULT 2

US-09-816-744-18
;; Sequence 18, Application US/09816744
;; Patent No. 6579520
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Jian
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Li, Hanzhong
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Tomas, Daniel
;; APPLICANT: VanLookeren, Menno
;; APPLICANT: Vandlen, Richard
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William
;; APPLICANT: Yansura, Daniel
;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;; FILE REFERENCE: PI381R1C1P2(US)
;; CURRENT APPLICATION NUMBER: US/09/816,744
;; CURRENT FILING DATE: 2001-03-22
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 18
;; LENGTH: 728
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-816-744-18

Query Match 92.3%; Score 3703; DB 4; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;
QY 42 RMKAARPRLCVANE-GVGPSARNISGLYNTTFKYDNCCTTYLNPVKGHVIAADAQNITISQY 100
DB 3 RASASGVPALFVSGEQGVGPASRNSGLYNTTFKYDNCCTTYLNPVKGHVIAADAQNITISQY 62
QY 101 ACHDQAVATILWSFGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSSFPKRTGME 160
DB 63 ACHDQAVATILWSFGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSSFPKRTGME 122
QY 161 SQPLNNKFTDYFVKVVPFPPSIKNESNYHPFPRTRACDILLQPDNLACKPFWKPRNLN 220
DB 123 SQPLNNKFTDYFVKVVPFPPSIKNESNYHPFPRTRACDILLQPDNLACKPFWKPRNLN 182
QY 221 ISQ-----HGSDMQVSFDHAPHNFGFRFFVLYHKLKHEGPFKRKTCQSQTT 267
DB 183 ISQHGSDMQVSFDHAPHNFGFRFFVLYHKLKHEGPFKRKTCQSQTT 242
QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302
QY 328 ATLFTVMCRKQKQENIYSHLDDESSSSTYTAALPRERLRPRPKVFLCYSSKQGNHNV 387
DB 303 ATLFTVMCRKQKQENIYSHLDDESSSSTYTAALPRERLRPRPKVFLCYSSKQGNHNV 362
QY 388 VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKK 447
DB 363 VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKK 422
QY 448 NYKHGGGRSGKGEFLVAVSAIAEKLRAQKQSSAALSFKFIAYVFDYSCGQVPGILD 507
DB 423 NYKHGGGRSGKGEFLVAVSAIAEKLRAQKQSSAALSFKFIAYVFDYSCGQVPGILD 482
QY 508 LSTKYRLMDNLPLQCSHLHSDHGLQBPQHTQGRSRNRYFRSKSGRSLYVAICNMHQFI 567
DB 483 LSTKYRLMDNLPLQCSHLHSDHGLQBPQHTQGRSRNRYFRSKSGRSLYVAICNMHQFI 542
QY 568 DEEDPWFKEQVFPFPPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 627

Db 543 DEEDWFEKQVPPHPPPLRYREPVLKFDGSLVNDVMCKGPGESDFCLKVEAAVLGAT 602
Qy 628 GPADSQHSQGGLDQGEARPAALDGSAAQPLHTVKAGSPDMPRDSGIYDSSVPSSE 687
Db 603 GPADSQHSQGGLDQGEARPAALDGSAAQPLHTVKAGSPDMPRDSGIYDSSVPSSE 662
Qy 688 LSLPLMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADIGCRSYTDEL 747
Db 663 LSLPLMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADIGCRSYTDEL 722
Qy 748 HAVAPL 753
Db 723 HAVAPL 728

RESULT 3
US-08-620-694A-10

; Sequence 10, Application US/08620694A

; Patent No. 5869286

; GENERAL INFORMATION:

; APPLICANT: Yao, Zhengbin

; APPLICANT: Spriggs, Melanie

; APPLICANT: Fanelow, William

; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Apple, Version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/620.694A

; FILING DATE: 21 MARCH 1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/538,765

; FILING DATE: 7 AUGUST 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/410,535

; FILING DATE: 23 MARCH 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,695

; REFERENCE/DOCKET NUMBER: 2617-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)597-0430

; TELEFAX: (206)

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 866 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-620-694A-10

Query Match 7.8%; Score 312; DB 2; Length 866;

Best Local Similarity 23.1%; Pred. No. 3.8e-23;

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

Qy 69 NITFKYDNC--TYYLNPVGKHVIADAQNT-----ISQVACHDQ-----VAVTIILWS 113

Db 49 NCTVKNSTCLDSDWIHP-----RNLTSPSPKDLQQLHFAHTQQGDLFPVHAIEWT 99

Qy 114 -PGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSSFKRTGMSOPFLNMKETD 172
Db 100 LQTDASILYLEGAEALSVLQNTNRLCVR--FEFLSKLRHHRRWRRTFSHFV--VDPQOE 156
Qy 173 YFVKV--VPFSPKSNESYHPFFRTRACDLLLLQPDNLACK--PFWKPRNL----- 219
Db 157 YEVTVHLLPAPIPDGDPNHQSKNLFVDPDCEHARKMVTTPCMSSGSLWDP-NITVETLEAH 215
Qy 220 -----NISQHGSDMOVSFDHAPHNFGFRFFYLHYLKLKHEGPFPRKCTCKQBOQTETT 270
Db 216 QLRVSFTLWNSTHYQILLTSFFPHENHSCFEHMH-HIPAPRPEFHQRSNVLTLLNLK 274
Qy 271 SCLLQNVSPGDYIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAF 327
Db 275 GCCRHOVQIOIPFFSSCLNCLRHSAVSCEPMPDTPPEIPDYMWPLWYFVTGSIILLVG 334
Qy 328 ATLFTVMCRKKQENIYSHLDEESSESSTYTAALPRERLRPRP-----KVFLCYSSKQCN 383
Db 335 SVILLIVCMTWRLAGPGS---EKYSDDTKTDTGLPAADLIPPLKPKRWIYISA-DHPL 390
Qy 384 HMYVQCFAFYFLQDFCGCEVALDLDWEDPSLCREGREWV---IQIHSOFIIVVCSKG 439
Db 391 YVDVVLKFAQFLLTACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
Qy 440 MKYFVDKKNYKHKGG-----RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIA 491
Db 451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDGLFTAAANNMILPDFKR-----PACFGTYVV 501
Qy 492 VYF--DYSCGDVPGILDSTKYRLMDNLPLQCSHLHSRDHGLQBPQOHTROG---SRRNYF 548
Db 502 CYFSEVSCDGDVPLFGAAPRYPLMDRFEV--YFRIOLEMFQFGMRHVRVGEISGDNYL 559
Qy 549 RSKSGRLYVAICNMHOFIDEEPWF-----KQFVPPHPPPLRYREPVLEKFDGSL 600
Db 560 RSPGGRQIRALDRFRDMQVRCPDWFCENLYSADDQDAPSLDEEV-FEELPLP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE-----SQHGG 640
Db 618 VKRAPLVRE-PGSOACLAIDPLVGEEGAAVAKLEPHLQPRGQAPAPQLHTLVLAEEGA 676
Qy 641 LDQDGEARPALDGA--ALQ-----PLLHTVKGSPDMPRDSGIYDSSVPSSESLP 691
Db 677 LVAAVEPGLADGAAVRLALAGEGEACPLGSPGAG-----RNSVLF--LPVDPEDSP 727
Qy 692 LMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGC 740
Db 728 L--GSSIFPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGC 768

RESULT 4

US-09-022-255-10

; Sequence 10, Application US/09022255

; Patent No. 6072033

; GENERAL INFORMATION:

; APPLICANT: Yao, Zhengbin

; APPLICANT: Spriggs, Melanie

; APPLICANT: Fanelow, William

; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Apple, Version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/022.255

220 -----NISQSGDMQVSDHAPHNFGFRFFYLHYLKLKHEGFFKRTCKOQTETT 270
216 QLRVSFTLWNESTHYQILLTSFPHWENHSCFEHMH-HI PAPRPEEFQORSNVTLTLNLK 274
271 SCLLQNVSPGDIYIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
275 GCCHQVQIOFPFSSCLNDCLRHSAIVSCPEMPDTPPIPYMPLWYWFITGISILLVG 334
328 ATLFTVMCRKQOENIYSHLDESESSSTYTAALPRERLRPR---KVFLCYSSKDQON 383
335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVMIIYSA-DHPL 390
384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREQREWV---IQKHESQFIIVVCSKG 439
391 YVDVVLKFAQFLLTACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
440 MKYFVDKKNYKHGGG-----RSGKGGLFLVAVSAIAEKLRQAKQSSAALSKEFIA 491
451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILLPDKR-----PACFGTYVV 501
492 VYF-DYSCGEGVPGILDSTKYRLMDNLQOLCSHLHSRDHGLQEPGQHTROG---SRRNYF 548
502 CYFSEVSCDGDVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGEISGDNYL 559
549 RSKGSRSLYVAICNMHOFIDEEPWFE-----KQFVPHPPPLRYREPVLKFDGSL 600
560 RSPGGRQLRAALDRFDWQVRCDFWFECEENLYSADDQDAPSLDEEV-FEEPLLP-GTGI 617
601 VLNDVMCKPGPESDFCLKVAAVLGATGPADSOHE-----SOHGG 640
618 VKRAPLVRE-PGSOACLAIDLVLGEGGAAVAKLEPHLQPRGQAPQPLHTLVLAEBGA 676
641 LDQGEARPALDGA---ALQ-----PLLHTVAGSPSDMPRDSIGIYDSSVPSSELSLP 691
677 LVAAVEPCPLADGAARVLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
692 LMEGLSTDTQTTSSITSVSSSGSGLEGEPPALPSKLLSSGCKADLGC 740
728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 6

US-08-978-773-4
; Sequence 4, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Trout, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2623-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-978-773-4

Query Match 7.8%; Score 312; DB 3; Length 866;
Best Local Similarity 23.4%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
QY 69 NITFYKDNQ--TTLNPNVGVKHVIADAQONIT-----ISQYACHDQ-----VAVTILWS 113
DB 49 NCTVKNSTCLDDSWIHP-----RNLTPSPKDLQIQLHFAHTQOGLFPVAHLEWT 99
QY 114 -PGALGIEFLKGFVRVILEELKSEGRQCQQLIKDPKOLNSFKRTGMESQPFLLNMKPTD 172
DB 100 LQTDASLTLYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDQE 156
QY 173 YFVKV--VPPPSIKNESYHPFFRTRACDILLQPDNLACK---PFWKPRNL-----219
DB 157 YEVTVHRLPKPIPDGDPNHQSKNPLVPDCEHARMKVTTTCMSSGSLWDP-NITVETLEAH 215
QY 220 -----NISQSGDMQVSDHAPHNFGFRFFYLHYLKLKHEGFFKRTCKOQTETT 270
DB 216 QLRVSFTLWNESTHYQILLTSFPHWENHSCFEHMH-HI PAPRPEEFQORSNVTLTLNLK 274
QY 271 SCLLQNVSPGDIYIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 275 GCCHQVQIOFPFSSCLNDCLRHSAIVSCPEMPDTPPIPYMPLWYWFITGISILLVG 334
QY 328 ATLFTVMCRKQOENIYSHLDESESSSTYTAALPRERLRPR---KVFLCYSSKDQON 383
DB 335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVMIIYSA-DHPL 390
QY 384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREQREWV---IQKHESQFIIVVCSKG 439
DB 391 YVDVVLKFAQFLLTACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
QY 440 MKYFVDKKNYKHGGG-----RSGKGGLFLVAVSAIAEKLRQAKQSSAALSKEFIA 491
DB 451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILLPDKR-----PACFGTYVV 501
QY 492 VYF-DYSCGEGVPGILDSTKYRLMDNLQOLCSHLHSRDHGLQEPGQHTROG---SRRNYF 548
DB 502 CYFSEVSCDGDVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGEISGDNYL 559
QY 549 RSKGSRSLYVAICNMHOFIDEEPWFE-----KQFVPHPPPLRYREPVLKFDGSL 600
DB 560 RSPGGRQLRAALDRFDWQVRCDFWFECEENLYSADDQDAPSLDEEV-FEEPLLP-GTGI 617
QY 601 VLNDVMCKPGPESDFCLKVAAVLGATGPADSOHE-----SOHGG 640
DB 618 VKRAPLVRE-PGSOACLAIDLVLGEGGAAVAKLEPHLQPRGQAPQPLHTLVLAEBGA 676
QY 641 LDQGEARPALDGA---ALQ-----PLLHTVAGSPSDMPRDSIGIYDSSVPSSELSLP 691
DB 677 LVAAVEPCPLADGAARVLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
QY 692 LMEGLSTDTQTTSSITSVSSSGSGLEGEPPALPSKLLSSGCKADLGC 740
DB 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 7

US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305

Db 451 TR-----AKWALLGAPVRLRCDHGXPGVGLFTAAAMNMLPDKFR-----PACFGYV 501
Qy 492 VYF-DYCEGVPGLDLSTKYRLMDNLPOLCSHLHSDHGLQEPGQHTROG--SRNYF 548
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 549 RSKGRSLYVAICNMHQFIDEEPWFE-----KQVPHPPPLRYRBPVLEKFDGL 600
Db 560 RSPGGRQLRAALDRFRDQVRCDFWECENLYSADDDQAPSLDBEV-FEPLLP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSHE-----SQHGG 640
Db 618 VKRAPLVRE-PSQAACLAIDPLVGEEGAATAKLEPHLQPRGPAPQPLHTLVLAEEGA 676
Qy 641 LDQGEARPALDGA---ALQ-----PLHTVKGSPSDMPRDSGIYDSVPSSELSLP 691
Db 677 LVAAVEPGPLADGAARLALAGEGACPLLGSPGAG-----RNSVLF--LPVDPEDSP 727
Qy 692 LMEGLSTDQETSTSLTESVSSSSGLGEEPPALPSKLLSGSKADLGC 740
Db 728 L--GSSTPMASPDLLPEDVR-----BHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 10

US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-257-10

Query Match 7.8%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
Qy 69 NITFKYDNC--TTYLNPVGKHVIADQNIT-----ISQYACHDQ-----NAVITLMS 113
Db 49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDLQIQLHFAHTQOGDLFPVAHIEWT 99
Qy 114 -PGALGIEFLKGRVRIEELKSEGRQCOQLILDKPOLNSSFRTKMGESQFFLNMKETD 172
Db 100 LQTDASILYLEGAEALSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFHFV-VDPQE 156
Qy 173 YFVKV--VPPPSIKNESNHPFFFRACDILLQONLACK--PFWKPRNL-----219
Db 157 YEIVVHLPKPIPDGPNHOSKNFLVPDCEHARKVTTPCMSSGSLWDP-NITVETLEAH 215
Qy 220 -----NISQHGSDMVQSFDPHAPNFGFRFFLYHLKHEGPPFKTKCKOQTTETT 270
Db 216 QLRVSFTLWNSTHYQILLTSFPHMENHSCFEHM-HIPAPRPEEFHQRNSVTLTLNLK 274
Qy 271 SCLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVLSAF 327
Db 275 GCCRQHQVQIQQFFSSCLNCLRHSAIVSCPEMPDTPPIPDYMPLWYWFITGISILVG 334
Qy 328 ATLTVMCRKKQENIYSHLDESSSTVTAALPRERLRPR-----KVFLCYSSKDGQN 383
Db 335 SVILLIVCMTWRLAGPS---EKYSDDTKYTDGLPAADLPPPLKPKRWIIYSA-DHPL 390
Qy 384 HNVVQCFAFYLDQFCGEVALDWDPSLCREGREW----IQKIHESQFIIVVCSKG 439
Db 391 YVDVLKFAQFLLTACGTEVALDLEBQAISEAGVMTWVGROKQEMVESNKIIVLCRG 450
Qy 440 MKYFVDKQNYKHGGG-----RSGKGEFLVAVSAIAEKLROAKQSSSAALSFA 491
Db 451 TR-----AKWQALLGRCAPVRLRCDHGXPGVGLFTAAAMNMLPDKFR-----PACFGYV 501
Qy 492 VYF-DYCEGVPGLDLSTKYRLMDNLPOLCSHLHSDHGLQEPGQHTROG--SRNYF 548
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 549 RSKGRSLYVAICNMHQFIDEEPWFE-----KQVPHPPPLRYRBPVLEKFDGL 600
Db 560 RSPGGRQLRAALDRFRDQVRCDFWECENLYSADDDQAPSLDBEV-FEPLLP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSHE-----SQHGG 640
Db 618 VKRAPLVRE-PSQAACLAIDPLVGEEGAATAKLEPHLQPRGPAPQPLHTLVLAEEGA 676
Qy 641 LDQGEARPALDGA---ALQ-----PLHTVKGSPSDMPRDSGIYDSVPSSELSLP 691
Db 677 LVAAVEPGPLADGAARLALAGEGACPLLGSPGAG-----RNSVLF--LPVDPEDSP 727
Qy 692 LMEGLSTDQETSTSLTESVSSSSGLGEEPPALPSKLLSGSKADLGC 740
Db 728 L--GSSTPMASPDLLPEDVR-----BHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 11

US-09-549-679-10
; Sequence 10, Application US/09549679
; Patent No. 6680057
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICANT: US/09/549,679
FILING DATE: 14-Apr-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE: <unknown>
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-549-679-10

Query Match 7.8%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFKYDNC--TTVLNVPVGHVIAQAQNI-----ISQYACHDQ-----VAVTILWS 113
DB 49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIWT 99
QY 114 -PGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQNSSFKRTGMSQFLNKKFETD 172
DB 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRWRFTFSHFV-VDPDQE 156
QY 173 YFVKV--VPFISIKNESNYHFFRTRACDILLQPDNLACK---PFWKPRNL-----219
DB 157 YEVTVHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTPPCSSGSLWDP-NITVETLEAH 215
QY 220 -----NLSQSGDMQVSFDHAPHNFGFRFFLYLHYKLHKGFPFKTKCKEQTTETT 270
DB 216 QLRVSFTLWNESTHYQILLTSFPHMNSHSCFEHMH-HIPAPRPEEFHORSNVTLLRNK 274
QY 271 SCLLQNVSPGYIYIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 275 GCCRHOVQIQPFSSCLNDCLRHSAIVSCPEMPDTPPEIPDYMWPLWYWFITGISILVG 334
QY 328 ATLFTVMCRKQOENIYSHLDESESTYTAALPRELRPRP-----KVFLCYSSKQGN 383
DB 335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVMYIYSA-DHPL 390
QY 384 HMNVQCFAYFLQDFCGCEVALDLEDESLCREQEWV---IQKIHESQFIIVVCSKG 439
DB 391 YDVVVLKFAQLLTACGTEVALDLLEEQAISEAGVMTWVGKQKQEWESNSKIIVLCRSG 450
QY 440 MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLQAKQSSAALSKEFTA 491
DB 451 TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMLPDFKR-----PACFGTYV 501
QY 492 VYF-DYSCGDPVPGILDSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTROG--SRNYF 548
DB 502 CYFSEVSCDGVPLDFGAAPRYPLMDRFEV--YFRIQDLEMFQPGRMHRVGLSGDNYL 559
QY 549 RSKGRSLYVACNMQHFDIEPDWFE-----KQFVFPHPPLRYREPVLKFDSCGL 600

DB 560 RSPGGRQLRAALDRFRDWQVRCDFWECENLYSADDQDAPSLDEEV-FEPLLLPP-GTGI 617
QY 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHE-----SOHGG 640
DB 618 VKRAPLVRE-PGSOACLAIDPLVGEEGAATAVAKLEPHLQPRGQAPQPLHTLVLAEBEGA 676
QY 641 LDQGEARPALDQSA---ALQ-----PLAHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 691
DB 677 LVAAVEGPLADGAARLALAGEGEACPLLGSPGAG-----RNSVLFF---LPVDPEDSP 727
QY 692 LMEGLSTDQETSTSLTESVSSSGLGEEPPALPSSKLLSSGSKADLGC 740
DB 728 L--GSSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGC 768
RESULT 12
US-10-033-522-1
Sequence 1, Application US/10033522
Patent No. 6793919
GENERAL INFORMATION:
APPLICANT: MOHLER, Kendall M.
TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists
FILE REFERENCE: 2982-A
CURRENT APPLICATION NUMBER: US/10/033,522
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 60/241,230
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 866
TYPE: PRT
ORGANISM: Homo sapiens
US-10-033-522-1

Query Match 7.8%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
QY 69 NITFKYDNC--TTVLNVPVGHVIAQAQNI-----ISQYACHDQ-----VAVTILWS 113
DB 49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIWT 99
QY 114 -PGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQNSSFKRTGMSQFLNKKFETD 172
DB 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRWRFTFSHFV-VDPDQE 156
QY 173 YFVKV--VPFISIKNESNYHFFRTRACDILLQPDNLACK---PFWKPRNL-----219
DB 157 YEVTVHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTPPCSSGSLWDP-NITVETLEAH 215
QY 220 -----NLSQSGDMQVSFDHAPHNFGFRFFLYLHYKLHKGFPFKTKCKEQTTETT 270
DB 216 QLRVSFTLWNESTHYQILLTSFPHMNSHSCFEHMH-HIPAPRPEEFHORSNVTLLRNK 274
QY 271 SCLLQNVSPGYIYIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 275 GCCRHOVQIQPFSSCLNDCLRHSAIVSCPEMPDTPPEIPDYMWPLWYWFITGISILVG 334
QY 328 ATLFTVMCRKQOENIYSHLDESESTYTAALPRELRPRP-----KVFLCYSSKQGN 383
DB 335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVMYIYSA-DHPL 390
QY 384 HMNVQCFAYFLQDFCGCEVALDLEDESLCREQEWV---IQKIHESQFIIVVCSKG 439
DB 391 YDVVVLKFAQLLTACGTEVALDLLEEQAISEAGVMTWVGKQKQEWESNSKIIVLCRSG 450
QY 440 MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLQAKQSSAALSKEFTA 491
DB 451 TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMLPDFKR-----PACFGTYV 501
QY 492 VYF-DYSCGDPVPGILDSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTROG--SRNYF 548

Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 549 RSKSGRSIYVAICNMHOFIDEEPWFEE-----KQFVPPHPPPLRYRREPVLEKFDGSL 600
Db 560 RSPGGRQJRAALDRFRDQVRCDFWFECEENYSADDOAPSLDEEV--FEEPLLP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHE-----SQHGG 640
Db 618 VKRAPLVRE--PGSOACLAIDLPLVGEEGA-AVAKLEPHLQPRQPAPQPLHTLVLAABEGA 676
Qy 641 LDQGEARPALDGA---ALQ-----PLLHTVKAGSPDMRDSGIVDSVPSSELSLP 691
Db 677 LVAAVEPGPLADGAARLALAGEAGEACPLLGPAG-----RNSVLF--LPVDPEDSP 727
Qy 692 LMEGLSTDQITSTISLTVSSSSGLGEEPPALSKLLSGSCCKADLGC 740
Db 728 L--GSSTPMASPDLLPEDVR-----BHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 13

US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-620-694A-2

Query Match 7.6%; Score 306; DB 2; Length 864;
Best Local Similarity 22.5%; Pred. No. 1.6e-22;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;
Qy 40 GWRM-----KAAARPREL-----CVANEGVGPSARNSGLYNITFKYDNCCTTYLNPVGK 86

Db 17 GWLLLLNLVLAAPGRASPRLLDFPAPVCAQEGSLCRVKNSTCLDDSWIHPKMLTSPSPKNI 76
Qy 87 HVTADAQNIITISQYACHDQAVT--ILWS--FGALGIEELKGFVILEELKSEGRQCOQ--- 141
Db 77 YI-----NLSVSTQHGELVPVLHVEWTLQTDASILEGAELSVLQNLNERLCVRFQF 131
Qy 142 --LILKDPKOLNSFKRTGMESQPFILNMKPFETYFVKVPFPSPKINESNYHPFFRTRAC 199
Db 132 LSWLQHRKWRFSF-----SHFVDPGQGEYEVTVHHLKPIPDGDPNHKSKILFVPDC 185
Qy 200 D---LLLPQNDLACKPFWKPRNLNI-----SQH-----GSDMQV 230
Db 186 EDSMKMTTSCVSSGSLMDP--NITVETLDTQHLRVDFTLWNESTPYQVLLSFSDSENHS 244
Qy 231 SFD-----HAPNFGFRFFYLHYKLKHE---GPFKRTCKQEQTTTTCLL 274
Db 245 CFDVVKQIFAPRQEFHQANVTTLTKFHWCCHHVQVQFF--FSSCLND-----CLR 296
Qy 275 QNVSPGDYIITELVDDTNTTRKVMHYALKPV--HSP--WA-GPIRAVAITVPLVISAFTL 330
Db 297 HAVTVPCVI-----SNTT-----VPRVADYIPLWYGLITLIAL-----LLVGSVIVL 341
Qy 331 FTVMCRKKQENIYSHLDESESSYTAALPRERLPRKPVFLCYSSKQGNHNVQC 390
Db 342 IICMTWELSGADQEKHGDDSKINGILPVADLTTPPLRPR--KWIVYSA--DHPLYVEVVLK 399
Qy 391 FAYFLQDFCCCEVALDLWEDFSLCREQREWVTK-----THESQFIIIVCSKGMKYFVDK 446
Db 400 FAQFLITACGTEVALDLLEBQVISEVGVMTWVRQKQEMVESNSKIIILCSR-----TQ 454
Qy 447 KNYKHGG-----GRSGKGELFLVAVSAIAEKLQAKQSSAALSKEFTAVYFDY 496
Db 455 AKWKAILGWAEPVQLRCDHWKPGADLFTAMNWLIPDKR-----PACFTYVVCYFSG 509
Qy 497 SC--EGDVPGLDLSTKYRLMDNLPLQCSHLHSDRHGLOEFGQ--HTROGSRNRYFRSKG 553
Db 510 ICSERDVDFLNTITSRYPLMDRFEV--YFRIQDLEMFQGRMHRVRELTDGNYLQSPSG 567
Qy 554 RSLYVAICNMHOFIDEEPWFQFVFFHP-----PPLR---YREPVLEKDSGLAVNDVM 606
Db 568 RQLKEAVLRFQEWQTCQDFWFERENCLADGQDLPSLDEEVFEDPLLP--GGGIVKQOPL 626
Qy 607 CKPGESDFCLKVEAAVLGATGPADSOHESQHGGLDQD-----GEAR 648
Db 627 VREL--SDGCLVVDVCV-----SEESRMAKLDPQLWFPQRELVAHTLQSMVLPAEQV 677
Qy 649 PALDGSAAQLPLHTVKAGSPSDMP--RDS-----GIYDSSV---FSSLSLPL----- 692
Db 678 PA---AHVVEPLHLPDGSGAAALPMTEDSEACPLLGVQRNSILCLPVDSDDLPLCSTPM 734
Qy 693 -----MEGLSTDQITSTISLTVSSSSGLGEEBPP-----ALPSKLLSSGSCCKADLG 739
Db 735 MSPDHLQGDAREQLESLMLSVLQOQSLSGPLESWPREVVLGCTPSEEBQQRQSVQSDQG 794

RESULT 14
US-09-022-255-2
; Sequence 2, Application US/0902255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-2

Query Match 7.6%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 1.6e-22;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;

QY 40 GWRM-----KAAARPRL-----CVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGK 86
DB 17 GWLLLLLVNAPGRASPLDFFAPVCAQEGSLCRVKNSTCLDSDSWHPKNTLTPSSPKNI 76
QY 87 HVIADAQNITISQVACHDOQAVT-ILMS-PCALGIEFLKGRVRLIEELKSGRCQQ---141
DB 77 YI-----NLSVSTQHGLVPLVHVEWTQDASILYLEGAELSVLQNTNRLCVKRFQF 131
QY 142 --LILKPKQLNLSFKRTGMSQPLANKFTDIFVKVPPSPKNSNYHPFFRTRAC 199
DB 132 LSLMLQHRKWRFSF-----SHFVVDPGQYEVTVHHLPKPIPDGDPNKHKIIIFVDC 185
QY 200 D---LLLPQDNLACKPFKPRNLNI-----SQH-----GSDMQV 230
DB 186 EDSKMKMTTSCVSGSLMDP-NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
QY 231 SFD-----HAPHNFGFRFFYLHYKLKHE---GPFKRKTKQEQTETTSCLL 274
DB 245 CFDDVVKQIFAPRQEFHQANVTFLSKFHCCHHVQVQPF-FSSCLND-----CLR 296
QY 275 QNVSPGDVIELVDNTTRKMHVALKPV--HSP-WA-GPIRAVAITVPLVLSAFATL 330
DB 297 HAVTVPCSVI-----SNTT-----VPRPVAADYIPLWYVGLITLAI-----LLVGSVIVL 341
QY 331 FTWCRKQKQENIYSHLDESESSSTYTAALPRBLRPRPKPVFLCYSSKSGQGNHNVQC 390
DB 342 ICTWRLUGADQEKHGDDSKINGILLPVADITPPPLRPR-KWIVYSA-DHPLVEVVLK 399
QY 391 FAYFLQDFCGCEVALDLWEDFSLREGQREWIQK-----IHESQFIIVVCSKGMKYFVDK 446
DB 400 FAQFLITACGTETVALDLLEEQVISEVGYMTWVRQKQEWESNSKIILCSR-----TQ 454
QY 447 KNYKHKG-----GROSGKGLFLVAISAETKLRQAKQSSSAALESKFTAVFYDY 496
DB 455 AKWKAILGWAEPAVQLRCDHWKPADGLFTAAMNMLPDKR-----PACFGTYVVCYFSG 509
QY 497 SC-EGDVFGILLDTKYRLMDNLPLQCSHLHSRDHGLQEPGQ--HTRQGSRRNRYFRSKSG 553

Db 510 ICSERDVPDLFNITSRYPLMDREFEV--YFRIQDLEMFEPGRMHVRELTDGNTYLOQSPSG 567
QY 554 RSLYVAICNMHOFIDBEPDWFKEQFVFFHB---PPLR---YREPVLKEFDSGLIVLNDVM 606
DB 568 RQLEAVLRPQEWQTCQPDWFERENICLADQDLPSLDBEVFEDPLLP--GGGIVKQOPL 626
QY 607 CKPGPESDFCLKVEAAVLTGATGPADSOHESQHGLDQD-----GEAR 648
DB 627 VRELPSDGLVVDVCV-----SEESERMAKLDLPQLWPQRELVAHTLQSMVLPAEQV 677
QY 649 PALDGSAALOPLLHTVKAGSPSMP--RDS-----GIYDSSV---PSSLSLPL-----692
DB 678 PA---ARVVEPLHLPDGSAAQLPMTEDSEACPILGQVRNSILCLPVDSDDLPLCLCTPM 734
QY 693 -----MEGLSTDQTTSSLTSSVSSSSGLCEBPP-----ALPSKLLSSSGCKADLG 739
DB 735 MSPDHLOGDAREQELSLMLSLVQOOSLSGQPLESWPRFVLEGTFFSEERQSVQSDQG 794

RESULT 15
US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-696-2

Query Match 7.6%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 1.6e-22;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;
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QY 40 GWRM-----KAAAPREL-----CVANEGVGPA SRNSGLYNTFKYDNCCTYLNVPVK 86
Db 17 GWLLLLNLVAPGRASRLLDFFAPVCAQEGLSCEVXNSCLDDSWIHPKMLTPESSPKNI 76
QY 87 HVIADAQNITISQYACHDQAVT-ILMS-PCALGIEFLKGRVILEELKSEGRQCOQ---141
Db 77 YI-----NLSVSTQHGBELVPLHVEMTLOTDASILYLEGAELSVLQNTNERLCVKQFQ 131
QY 142 --LILKDPKQLNSSFKTKMESQFELNMKFETDYFVKVPPSPKKNESNYHPFFRTRAC 199
Db 132 LSQLQHRKRWRFSGF-----SHFVDPDQGEYEVTVHHLPKPIPDGDPNHKSKIIFVDC 185
QY 200 D---LLLPQDNLACKPFWKPNLNI---SOH-----GSDMQV 230
Db 186 EDSKWKMTTSCVSGSLWDP-NITVELDTQHLRVDFTLWNESTPYQVILLESFSDSENHS 244
QY 231 SFD-----HAPHNFGFRFFLYHLKXHE---GPPKRKCKQEQTETTTSCLL 274
Db 245 CFVVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHVQVQPF-FSSCLND-----CLR 296
QY 275 QNVSFGDYIIELVDDTWTTRKMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330
Db 297 HAVTVPCFVI-----SNTT-----VPKPVADYIPLWVYGLITLIAI-----LLVGSVIVL 341
QY 331 FTVNCRKKQENIYSHLDESSSESTVTAALPRERLRPRPKVFLCYSSKDGQNHMNVQC 390
Db 342 IICMTWRLSGADQEKHGDDSKINGILPVADLTTPPLRPR-KWIVYSA-DHPLYVEVVLK 399
QY 391 FAYFLQDFCGCEVALDLMEDFSLCREGQREWVIOK----IHESQFIIVCCKGMYFVDK 446
Db 400 FAQLITACGTGEVALDLLEEQVISEVGVTWVSQKQEMVESNSKIILCSRG-----TQ 454
QY 447 KNYXHKGG-----GRSGKGELFLVAVSAIAEKLRQAKOSSAALSKEFTIANYFDY 496
Db 455 AKWKAIIIGWABPAVOLRCDHWKPAQDLFTAMNMILPDKR-----PACFTYVVCYFSG 509
QY 497 SC-EGDVPGLDLSTKYRLMDNLPLQCSHLHSRDHGLQEPQO--HTRQSGRRNYFRSKSG 553
Db 510 ICSEKVPDLFNITRYPLMDRFEV--YFRIQLEMFEPGRMHVRELTDGNYLQSPSG 567
QY 554 RSLYVAICNMHQFIDEBPDWFEPKQFPFHP-----PPLR---YREPVLKFDGSLVLDNMV 606
Db 568 RQLKEAVLRFQEWOTQCPDWFERENCLADGQDLPSLDEEVFEDPLPP-CGGIVKQOPL 626
QY 607 CKPGPESDFCLKVTAANVLGATGPADSOHESQHGGLDQD-----GEAR 648
Db 627 VRELFP-SDGLVVDVVCV-----SEESERMAKLDPLQWPQRELVAHTLQSMVLPAEQV 677
QY 649 PALDGSAAALQPLLHTVKAGSPDMP--RDS-----GIYDSSV---PSSLSLPL-----692
Db 678 PA---AHVVEPLHLPDGSAAAQPLMTEDSEACPILGVQRNSILCLPVDSDDLPLCSTPM 734
QY 693 -----MEGLSTPDQETSLTESVSSSGLGEEPPP-----ALPSKLLSSGSKADLG 739
Db 735 MSPDHLQGDAREQLESMLSVLQSLGQPLESWPRPEVVLGCTPSEEEQORSQVQSDQ 794
```

Search completed: August 9, 2005, 11:51:08
Job time : 42.7138 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:37:17 ; Search time 30.2019 Seconds
(without alignments)
2398.896 Million cell updates/sec

Title: US-10-717-282-2
Perfect score: 4013
Sequence: 1 MAPWLQCSVPFTVNACLNG.....CKADLGCRSYDELHVAAPL 753

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3005	74.9	564	2 T42695	hypothetical prote
2	170.5	4.2	846	2 T27282	hypothetical prote
3	126.5	3.2	718	2 T30113	hypothetical prote
4	117	2.9	757	2 T09081	telomere-associate
5	117	2.9	917	2 T04661	hypothetical prote
6	117	2.9	2946	2 T00867	hypothetical prote
7	116.5	2.9	901	2 F83781	transposase (08) /
8	115.5	2.9	938	2 I49071	protein kinase - m
9	115	2.9	998	2 S37627	protein-tyrosine k
10	110	2.7	535	2 T17212	hypothetical prote
11	110	2.7	592	2 I49239	vesicle transport
12	108.5	2.7	3788	2 T13960	beige protein, homo
13	107.5	2.7	3942	2 T42730	Basoon protein -
14	107	2.7	3788	2 T30851	lysosomal traffick
15	106.5	2.7	638	2 D86477	protein F1504.27 l
16	106	2.6	1448	2 A12007	Subtilase family p
17	105	2.6	901	2 JC5093	dead ringer nuclea
18	105	2.6	1571	2 T14155	zinc finger protei
19	104	2.6	1462	1 B36182	protein-tyrosine-p
20	103.5	2.6	663	2 A39897	GTFase-activating
21	103.5	2.6	930	2 A84668	Argonaute (AGO1) -1
22	102	2.5	813	2 B47485	ABR protein 2 - hu
23	102	2.5	859	2 A49307	98K GTFase-activat
24	101.5	2.5	822	2 A47485	ABR protein 1 - hu
25	101.5	2.5	1639	2 T50119	probable sensory t
26	101	2.5	641	2 T05497	hypothetical prote
27	101	2.5	664	2 T51247	ARR2 protein limpo
28	101	2.5	1275	2 A39885	nucleotide exchang
29	100.5	2.5	938	2 T05533	hypothetical prote

30	100.5	2.5	974	2 B59434	Rho GTPase activat
31	100.5	2.5	1007	2 T24643	hypothetical prote
32	99.5	2.5	657	2 E96949	serine/threonine p
33	99.5	2.5	794	2 S59069	z13 protein - mous
34	99.5	2.5	981	1 POMVGM	gag-abl polyprotei
35	99	2.5	341	2 H71716	190 kd antigen pre
36	99	2.5	783	2 A31491	sex-determining re
37	99	2.5	970	2 S63059	hypothetical prote
38	98.5	2.5	353	2 T33782	hypothetical prote
39	98.5	2.5	963	2 AD2381	type I site-specif
40	98.5	2.5	993	2 T48653	mouse developmenta
41	98.5	2.5	1050	2 G86582	exodeoxyribonuclea
42	98.5	2.5	1050	2 H72041	exodeoxyribonuclea
43	98.5	2.5	1050	2 C91624	hypothetical prote
44	98	2.4	526	2 T16124	hypothetical prote
45	98	2.4	820	2 S33794	hypothetical prote

ALIGNMENTS

RESULT 1

T42695
hypothetical protein DKFp434N1928.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42695
R:Bloecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A:Reference number: Z22230
A:Accession: T42695
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-564 <AAA>
A:Cross-references: UNIPROT:Q9UFA0; EMBL:AL133097
A:Experimental source: adult testis; clone DKFp434N1928
C:Genetics:
A:Note: DKFp434N1928.1

Query Match 74.9%; Score 3005; DB 2; Length 564;
Best Local Similarity 99.8%; Pred. No. 1.9e-232;
Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	190	HPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDFHAPNFGRFFFLHYK	249
Db	1	HPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDFHAPNFGRFFFLHYK	60
Qy	250	LKHEGPPFRKTKCKOEQTTEITSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA	309
Db	61	LKHEGPPFRKTKCKOEQTTEITSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA	120
Qy	310	GPIRAVAITVPLVVISAFATLFTVMCRKQQENIYSHLDESSSESTYTAALPRRLRPR	369
Db	121	GPIRAVAITVPLVVISAFATLFTVMCRKQQENIYSHLDESSSESTYTAALPRRLRPR	180
Qy	370	PKVFLCYSSKDGQNHMVVQCFAYFLQDFCCGEVALDLWEDFSLCREGQREWVIQKHES	429
Db	191	PKVFLCYSSKDGQNHMVVQCFAYFLQDFCCGEVALDLWEDFSLCREGQREWVIQKHES	240
Qy	430	QFIIVVCSKGMKYFVDKKNYKHGGGRSGKGEFLVAVSAIAEKLRAQKSSSAALSXF	489
Db	241	QFIIVVCSKGMKYFVDKKNYKHGGGRSGKGEFLVAVSAIAEKLRAQKSSSAALSXF	300
Qy	490	IATVFDYSCGDPVPGILDSTKYRLMDNLPLQCSHLHSRDHGLQFPQGHTRGSRNRYR	549
Db	301	IATVFDYSCGDPVPGILDSTKYRLMDNLPLQCSHLHSRDHGLQFPQGHTRGSRNRYR	360
Qy	550	SKSGSLVVAICNMHQFIDEEDPMFEKQFVPHPPPLRYREPVLEKFDGLVNDVMCKP	609
Db	361	SKSGSLVVAICNMHQFIDEEDPMFEKQFVPHPPPLRYREPVLEKFDGLVNDVMCKP	420
Qy	610	GPESDFCLKVEAAVLGATGPADSQHESQHGGLDQGEARPALDGSAAALQPLLHTYKAGSP	669

A;Reference number: Z16557; MUID:98198830; PMID:9539423
A;Accession: T09081
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-757 <S>
A;Cross-references: UNIPROT:O13399; EMBL:AF030885; NID:g2642221; PID:g2642222
A;Experimental source: strain FB2
C;Genetics:
A;Gene: UTASrecQ
C;Keywords: DNA binding

Query Match 2.9%; Score 117; DB 2; Length 757;
Best Local Similarity 20.4%; Pred. No. 0.63;
Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;

QY 268 ETTSCLIQNSPGDYIIELVDDTNTTRKVMHYALKPSPWAGFIRAV-----AITVPL-- 321
DB 77 ETITILIPTVALRANMLAKLDVN-----IRYHWQP-GSKKAAPIVLVSTEAATILAEKE 131
QY 322 -----VVISAFATLFTVMCRKKQQNNIYSHLDESESESSTYTAAALP----- 362
DB 132 YANRLLOQLDRIVIDECHELTILTARSYRRSMQLAMHVRDVTOTVWLTTATLPPIFEA 191
QY 363 --RELRPRPKVF-----LCYSSKDGGNHNVQCF-AYPELDPCGCEVALDLWEDF 411
DB 192 FISHNKLTKPLIVRESTNRSLCYSVRTAEHRSGMTCYDAVRVD---ECRARTDIW--- 246
QY 412 SLCREGQEWVIQIHESQFIIVVCCKGMKYFYDK-----KNYKHKGGRGS----- 458
DB 247 ----NGQRD-----RIIVYCTS--KELVARLAEMGLCAAYSESSEADKAAIIQ 290
QY 459 ----GKGELFLVAISAETAEKLRQAOKSSSAALSKFIAVYFDYSCEGDVPQIL--DLSTKY 512
DB 291 DWICGKSPVIVATSA-----LCGVGFDPHVRFVIIHLGPDLLITDF 331
QY 513 -----RLMDNLPOLCSHLHSRDHGLQEPGOHTQGSRNRYFS 550
DB 332 SQESGRAGRDCMPAESILLAGPQLDDRPA--ASKASSAEKGVAPG---ADKEAMQLYRS 387
QY 551 KSGRSLVAICNMHOVIDEPPDWPEKFQVFPFHPLPYREPVLKFDGSIVLNDVMCKPG 610
DB 388 RK----YCLRGVLSQLLDQRSW-----RWCMEGDQLCSVC 419
QY 611 PESDFCLKVEAAVLGATGPADSQH---ESQHGGLDQGEARPALDGSAALQPLLHTVKAG 667
DB 420 PGHHF-----QARGPGDQPFHTAPAQAQDPSTQCSRHPSSHMGSS--HPSMW----- 463
QY 668 SPDMRPDSGIYDSSVPSSE-LSLPLMEGLSTDOTETSSLTESVSSS---SGLGEEPPA 723
DB 464 -----GSSHPSSHGHSHPSIHGSS-HPSIHGSGOHGQRRKOQPD 510
QY 724 LPSK 727
DB 511 PPSE 514

RESULT 5
T04661
hypothetical protein F8D20.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04661
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes,
submitted to the Protein Sequence Database, July 1998
A;Reference number: Z15381
A;Accession: T04661
A;Molecule type: DNA
A;Residues: 1-917 <BE>
A;Cross-references: UNIPROT:O81789; EMBL:AL031135
A;Experimental source: cultivar Columbia; BAC clone F8D20
C;Genetics:
A;Map position: 4
A;Introns: 13/3; 58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3; 685/3;

Db 559 RCFWDSPEFIKSDGQVAFALFD--KLREGGENMIEVIDLSKTYRNQVW-----KGIN 612
Qy 442 YFVDKKNYKHGGGSGKGLFLVAVSAI-----AEKLRQAKQSSAALSK 488
Db 613 MFIEKGMVGLLPGNAGKSTTSMISLIQPTSGDVLIIKGGSIHKOSKAIRSLGVVPPQ 672
Qy 489 FIAYFYDSCB-----GDVPGILDLSKYLRLMDNLPLQCLSHLSHRDHGLQEPQOHTROG 542
Db 673 EIAVYHDLTARENLAFFGKIYGLGKEELKXR--MESTIQLV-----GLEE-----RQN 718
Qy 543 SRRNYFRSKSGRSYVAICNMHQ---FIDEEP 571
Db 719 DRVHTFGMKRRRLNIAVALLHEPELIIMDEP 750

RESULT 8
149071
protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149071
R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A:Title: Identification of novel protein kinases expressed in the myocardium of the deve
A:Reference number: 149071; MUID:95200798; PMID:7893599
A:Accession: 149071
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-938 <RES>
A:Cross-references: UNIPROT:Q60669; EMBL:U11493; NID:G595418; PIDN:AAA67925.1; PID:G5954
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:571-839/Domain: protein kinase homology <KIN>
F:579-587/Region: protein kinase ATP-binding motif
F:862-928/Domain: SAM homology <SAM>

Query Match 2.9%; Score 115.5; DB 2; Length 938;
Best Local Similarity 19.4%; Pred. No. 1.1; Mismatches 285; Indels 259; Gaps 45;
Matches 160; Conservative 120

Qy 9 SVFFTVNACL-NGSOLAVA-----AGGSGR---ARGADTCGWRMKAARPRLC----- 52
Db 170 SLVTAPRACIANAEVSVPLKLYCNGDGEWVPVVGACTCATGHEPAKESQCRACPPGSY 229
Qy 53 VANEGVGPA-----SRNSG-----LYNTFFKYN-----CTTYLNPVGHKVIADAQ 93
Db 230 KAKQEGPCPLCPPPNSRTTSPAASICTCHNNFYRADSDSADSACTTTRSP-PRGVISNV- 287
Qy 94 NITISQYACHQVAVTIILWS-PGALGIEFLKGFPRVILEELK-SEG-----ROCOQLIL 144
Db 288 -----NETSLILEWSEPRDLGRRDILLVYICKKCGSGGAGGATCSRCDNVE 337
Qy 145 KDPQLNSSFKRTGMESQFPLNMKPTDYFKVAVFPFSPISKNESNVHPFFFRTRACDILLQ 204
Db 338 FVPRLGLUTERLVHIS-----HLLAHTRYTEVQAVGVSGKSLPPRYAAVNTTNOAA 392
Qy 205 PDNLACKPFKRTGMESQFPLNMKPTDYFKVAVFPFSPISKNESNVHPFFFRTRACDILLQ 263
Db 393 PSEV-----PTLHSHSTSGSSLLTSLWAPPRPENG-----VILDYEMKY---FEKSKALAS 439
Qy 264 BQTTTTSCLLQNVSP-GDYIIELVDDTNTTKV-----MHYALKPVHSPWAGPIRAVA 316
Db 440 TVTSQKNSVQLDGLQPDARYVQV-----RARTVAGYQYTHPAEFETTSSRGSGAQQQL 494
Qy 317 ITVPLVITSAFA-----TLFTVMCKKQENIYSHLDESSSTYTALPRERLRP 368
Db 495 EQLPLIVGNSVAGFVFMVVVVVIAVCLRKQRH-----GPDAYTEKL-QOYTAP 543
Qy 369 RPKVFLCYSSKDGQNMNVVOCFAYFLQDFC-GCEVALDLMEDFSLCGREGREWYQIKH 427
Db 544 GNMKYIDFTYEDFN-EAVREFAKEIDVSCVKIEEVIGAGEFGEVCR----- 589

Qy 428 ESOFIIVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAI-----AEKLRQAKOSS 483
Db 590 -----GRLKLPGRREVF-VAIKTLKVGTYERQRDRDFLSEA 623
Qy 484 AALSKEITAVFYDSCBGPVIGILDLS---TKYR-----LMDNLPLQCLSHLSHRDHGLQ 533
Db 624 SNMGQF-----DHENIIRLEGVVTYKSPVPMILLTEFMENC-ALDSFLRLND----- 667
Qy 534 EPQOHT-----RQSSRRNY-FRSKSGRSLYV---AIC-----NMHQFIDE 569
Db 668 --GQFTVQLVGLMGLGIAAGMKYLSMNVYVHRDLAARNILVNSNLVCKVSDFGLSRFLD 725
Qy 570 EPDWFEKQF-----VPEH---PPPLRYREPVLKEDS-----GLVLDNMCKPGPE 612
Db 726 DPS--DPTTSSILGKIPIRWTAPEIAYR-----KFDASDVMSYGVIMWEVMS----- 773
Qy 613 SDFCLKVEAAVLGATGAPDSQHSQHGLDQDGEARFALDGSAAALQALLHTVTKAGSPSDM 672
Db 774 -----YGEQPYWNMSNQDDINAVEQDRLPPEPMDCTALHQLMASCWVRDRLNR 822
Qy 673 PRDSGIYD-----SSVPSSELSLPLMEGLSTDQ 701
Db 823 PKFSQIWNITLDKLIRNAASLKVTASAPSG-MSQPLLDRTVPDY 865

RESULT 9
S37627
protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37627
R:Boehme, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Streibhardt, K.; Ruebs
Oncogene 8, 2857-2862, 1993
A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.
A:Reference number: S37627; MUID:93390963; PMID:8397371
A:Accession: S37627
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-998 <BOE>
A:Cross-references: UNIPROT:P54753; EMBL:X75208; NID:9406867; PIDN:CAA53021.1; PID:94068
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki
F:631-899/Domain: protein kinase homology <KIN>
F:639-647/Region: protein kinase ATP-binding motif
F:922-988/Domain: SAM homology <SAM>

Query Match 2.9%; Score 115; DB 2; Length 998;
Best Local Similarity 19.0%; Pred. No. 1.4;
Matches 158; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

Qy 35 GADTCGWRMKAARPRLC-----VANEGVGPA-----SRNSG-----LYNTFFK 73
Db 267 GACTCATGHEPAKESQCRPCPGSYKAKQEGPCPLCPPPNSRTTSPAASICTCHNFFR 326
Qy 74 YDN-----CTTYLNPVGHKVIADAQNTISQYACHQVAVTIILWS-PGALGIEFLKGF 126
Db 327 ADSASDASACTVESP-PRGVISNV-----NETSLILEWSEPRDLGVRDLDLYN 374
Qy 127 VILEELKSEG-----ROCOQLILKDPQLNSSFKRTGMESQFPLNMKPTDYFKVAVFP 181
Db 375 VICKKCHGAGASACSRCDNVEFVPRLGLSEPRVHTS-----HLLAHTRYTEVQAVN 429
Qy 182 SIKNESNVHPFFFRTRACDILLQPDNLACKPFKWRPNLNIHQSGSDMVSFDPHAPNPGF 241
Db 430 GVSQKSLPPRYAAVNTTNOAASEV-----PTLHSHSSGSSLLTSLWAPPRPENG- 481
Qy 242 RFFYLHYKLHEGPF-KRKTCKQOQTETTSCLLQNVSP-GDYIIELVDDTNTTKVMHY 299
Db 482 --VILDYEMKY---FEKSEGIASITVSQNSVQLDGLRDPARYVQV-----RARTVAGY 531
Qy 300 A--LKPVH-----SPWAGPIRAVAITVPLVITSAFATL-----FTVMCKKQENIYS 345
Db 532 QOYSRPAEFTTSSRGSGAQQQLQEQPLIVGSATAGLVFVAVVIAVCLRKQRH----- 587

A;Reference number: Z17837
A;Accession: T13960
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3788 <MOR>
A;Cross-references: UNIPROT:Q922X9; EMBL:AB020019; NID:dl035670; PID:dl035670; PIDN:BA03
A;Experimental source: strain DA; spleen
C;Genetics:
A;Gene: beige

Query Match 2.7%; Score 108.5; DB 2; Length 3788;
Best Local Similarity 19.4%; Pred. No. 33;
Matches 144; Conservative 98; Mismatches 267; Indels 235; Gaps 38;

QY 20 GSQLAVAAGSGRARGADTCGRMKAAARPRLCVANEGVGVPASRNSGLYNITPKYDNCCT 79
DB 651 GETLQGLCGAGSPCGLPSPSYR-----QGILP-----SSSEDFLWKWDALAE 695
QY 80 YLNPVGKHVIADAQNIITISOVACH--DQVAVTILWSPGALGIEFLKGRFVILEELKSEG- 136
DB 696 YQNFIFOE--DRLHNTQIASHCNLIQKGNVIVQ-----KLYNYIFNPVLQGV 743
QY 137 ---RQCQOLIKDPKQLNSSFRTGMSQPFNNKFFET-DYFVKVP-----FP 181
DB 744 ELVHHCQQLSI-----TSAQTHMSGSQLKQYLPQEVLIQIYKLTPLILLKSRVIRDLFL 795
QY 182 SIKN-----ESNY-----HPP-FPRTACDLLQPDNLACKPFWKPRNLNISOHGSDMQ 229
DB 796 SCNGVNHIELNYLDGIRSHLSKAFETLIVSLGQQKRAAVPGV---DGLDIQELSSLS 852
QY 230 VSPFHAPHNFGFRFYHLKHEGPPFKTKCKEQTTETTSCLLQNVSPGDYIIELVDD 289
DB 853 V-----GPSLHK-----QQASTDPCSRLK-----FYASLRDT 880
QY 290 TMTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAPATLFTVMCKKQOENIYSHLDE 349
DB 881 DPKKRKTVHQ-----DAHINTINLFCVAF-----LCVSKAEDSDRESAN- 920
QY 350 ESSBSSTY--TAALPRELRPRPKVFLCYSSKDGQNHVV-----OCFAYFLQDFCGCEV 403
DB 921 ESEDTSGYDSTASEPLSHMLPRLSL-----ENVVLPSPCLHH-----958
QY 404 ALDLWEDFSLCREGQREWV--IQKHESQFI-----IVVCSKGMKYFVDKKNYKKGQGG 457
DB 959 AADIW-----SMCK-----WYMLNSVFOKQFHRLGQVQCHL-LIFMIIQKLFHSHTEQ 1009
QY 458 SGKGEFLF-----LVAVSAIAEKLRQAKQSSAALSKEFIAYVFDYSCEDGVPGILD----- 507
DB 1010 RQGEMSVNKGQGLMRIISQPEMLKEDVSSSTAPEPGFLKKSADRVSELESQHMLPTS 1069
QY 508 --LSTK-----YRLMDNLPLCSH-----LHSRDHGLQEPGQHTROG 542
DB 1070 QILATKSIPEBAKTFMNOSETCLQSIIRLESLLAICLHSARASQOKMELELPSQ----- 1124
QY 543 SRNRYFRSKSGSLYVALCNMHQFIDEF-----DWFEKQFVFPFPPPLRYRE 591
DB 1125 -----SLSENILCELDHLSQSKVAETELAKPLFDALRLVALGNHSAADLPDGT 1174
QY 592 VLEKFDGLVLDVNMCKGPESDFCLKVEAAVLGATG-----PADSQHESQHGGLDQDGE 646
DB 1175 VTEKSHPS---EVLVSQFGDTSFEAEEDSQCSLKLGLGEEGYEADSESNPEDGETQDDGV 1231
QY 647 ARPALDG--SAALQP--LLHTVKAG 667
DB 1232 ELPEAEGSGSIVPNLLESLLTHG 1255

RESULT 13
T42730
Bassoon protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42730

R;Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
A;Reference number: Z22249; MUID:98345363; PMID:9679147
A;Accession: T42730
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3942 <DIE>
A;Cross-references: UNIPROT:O88737; EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g341
A;Experimental source: strain 129 SVJ
C;Genetics:
A;Map position: 9F1
A;Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
A;Note: bassoon
C;Function:
A;Description: may be involved in cytomatrix organization at the site of neurotransmitter
A;Note: component of the presynaptic cytoskeleton
C;Keywords: coiled coil; zinc finger

Query Match 2.7%; Score 107.5; DB 2; Length 3942;
Best Local Similarity 19.1%; Pred. No. 43;
Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;

QY 516 DNLPLCASHLHSDHGLQEPGQHTROGSRNRYFRSKSGRSIYVAIC-----NMHQFIDEE 570
DB 3535 DTCFQFCS-----SHSMPDVQEHVKDGPRAHYKREEGYMLDDSHCVVSDSEATHLGOEE 3589
QY 571 PDMEKQFVFPFPPPLRYRE-----PVLEKF-----DSGLVLDVNMCKPG 610
DB 3590 TDMFDK---PRDARSDFRHHGGHTVSSSQKRGPARSHYDYPPEGLWPHD---EGG 3643
QY 611 PESDFCLKVEAAVLGATGPADSQHESQHG-----GLDQDG-----EARP- 649
DB 3644 PGRH-----TSAXEHRHSDHGRHSGRHAGEEPCGRRAAKPHARDMGREARPH 3691
QY 650 -----ALDGSALQPLLTHTV 664
DB 3692 PQASPAPAMOKGQGYFSSADYSQSSRAPSAHYHASESKKGSQAHTGPSALQPKADTQ 3751
QY 665 KAGSPDMPRDSGLYDSSVPSSSELSLPLMEGLSLTDQTETSLTSVSSSSGLGEEPPAL 724
DB 3752 AQPMQGRQAAPGQQSQPPSSRQT---PSGTASRQPTQOQQOQQOQQOGLGQAFOQA 3808
QY 725 PSK 727
DB 3809 PSQ 3811

RESULT 14
T30851
lysosomal trafficking regulator, long splice form - mouse
N;Alternate names: beige protein homolog
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30851
R;Barbosa, M.D.F.S.; Tchernev, V.T.; Kingmore, S.F.
submitted to the EMBL Data Library, September 1996
A;Description: two bg or not two bg? Longest isoform of mouse Lyst (beige) gene.
A;Reference number: Z20903
A;Accession: T30851
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3788 <BAR>
A;Cross-references: UNIPROT:P97412; EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AAC530
A;Experimental source: strain C57BL/6J
C;Genetics:
A;Gene: Lyst
A;Map position: 1
C;Keywords: alternative splicing

Query Match 2.7%; Score 107; DB 2; Length 3788;
Best Local Similarity 19.5%; Pred. No. 44;
Matches 156; Conservative 104; Mismatches 288; Indels 254; Gaps 44;

Qy 20 GSQLAAGGSGRGADTCGRMKAAPRLCVANEGVGPASRNSGLYNITFKYDNCCT 79
Db 651 GETLOGLTCGAGPTSGLPSYRF-----QGILP---SSGEDLLKWDALAE 695
Qy 80 YLNPVGKHVADANITISQVACH--DOVAVTIILSPGALGIEFLKGRFVILEBLKSEG- 136
Db 696 YQSFFVQF--DRLHNIQIANHICNLLQKGNVVQW-----KLYNIFNPVLQGV 743
Qy 137 ---RQCQOLILKDPKQLNSSPKRTMESQPLNKKFET-DYFVKVVP-----FP 181
Db 744 ELVHHCCQOLSIPS-----AQTHMCSQLKQYLPOEVLQIYLYLTPVLLKSRVIRDLFL 795
Qy 182 SIKN-----EGNY-----HPP-FPRTACDILLQPNLACKPFWKPRNLNISOHSDMQ 229
Db 796 SCGNVNHIEILNYLDGTRSHSLKAFETLIVSLGQQKDAVLDV---DGLDIOBELSLS 852
Qy 230 VSFDPHNFGRFFYLHYKLKHEGPFKRTCKOEQTETTSCLLONVSPGDYIIELVDD 289
Db 853 V-----GPSLHK-----QOASSDSPCSLRK-----FYASLREP 880
Qy 290 TINTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAPATLFTVMCKKKQENIYSHLDE 349
Db 881 DPKRKTTH---QDVH-----INTINLFLCVAP-----LCVSKHEADS---DR 916
Qy 350 ESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMVW---OCFAFYFLQDFCGCEVAL 405
Db 917 ESANESDTSYDPSPPSEPLSHMLPCLSLD-----VLPSPCLHH-----AA 960
Qy 406 DLWEDFSLCREGQREW--IOKIHESQFI---IWCCKGMKYFVDKKNYKHGGGRSG 459
Db 961 DIW---SMCR-----WIYMLNSVFQKQPHRLGGFQVCHE-LIFMIIOKLPFRSHTEQRR 1011
Qy 460 KBELF-----LVAVSAEAKLRQAKSSAALSKEFTAVYEDYSCBGDVPGL--DLSTK 511
Db 1012 QGEMSRNENQELIRIS-----YPELTKGDVSSATAPDLGL 1048
Qy 512 YRLMDN-----LPQLCSHLHSRDHGLQEPGQHTROGSRNRYFVSKSGSLYVAICN 562
Db 1049 RKSADSVNGFSGQVPLPFSAEQIVATE---SVPG-----RKAFMSQOSETSLQIRL 1098
Qy 563 MHQFIDEPDFWEKQFVFPFHPPLRYRREPVLKEKFDGLVLDNMCK-----608
Db 1099 LESLLD-----ICLHSARACQKQMLELPSQGLSVENILCELREHLSQSKVAETE 1148
Qy 609 -PGPESDFCLKVEAAVLGA-TGPADS-----QHESQHGGLDDGGEARPALDGSAAQLPLH 662
Db 1149 LAKPLFDALLRVLGNHSAIDLPGDAVTEKSHPSSEELLSPQGDPSSEAEQSQCSLKL 1208
Qy 663 TVKAGSPSDM---PRDSGIYDSSVPSSFSLPLMEGLSTQDTETSSLTESVSSSGLGE- 718
Db 1209 GEEGYEADSENEDVUTQDGV---ELN-PEAEGFS-GSIVSNLLENLTH-----GEI 1259
Qy 719 --EBPPALPSKLLSGSGCKADL 738
Db 1260 IYPEICMLGLNLSAKKLVD 1281

RESULT 15

D86477
protein F1504.27 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86477
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86477

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-638 <STO>

A:Cross-references: UNIPROT:Q9LQF8; GB:AB005172; NID:g8778345; PIDN:AAF79353.1; GSPDB:GN

C:Genetics:

A:Gene: F1504.27

A:Map position: 1

Query Match 2.7%; Score 106.5; DB 2; Length 638;

Best Local Similarity 19.4%; Pred. No. 3.4;

Matches 94; Conservative 63; Mismatches 175; Indels 153; Gaps 24;

Qy 94 NIITISQACHQDVAVTIILSPGALGIEFLKGRFVILEBLKSEGRCQOOLILKDPKQLNSS 153

Db 275 DIKYQVSYCHLODFCYVVS-----KCATHENYMDGKELEWETESDETDISP 322

Qy 154 FKRTMESQPLNKKFETDYFVKVVP---SIKNESNYHPFFRTRACDILLQPDNLAC 210

Db 323 FRNLG-----DGFIKHFKCHKHRLKLNHDGARDTEKQCEAC---IYP--IVS 364

Qy 211 KPFWKPRNLNISQHG--SDMQVSFDRHAPNFGFRFFYLHYKLKHEGP--FKRKTCKOEQT 266

Db 365 HQFVCHCKKNYSLHEVCAGLSRKLDDALHN-----HTLILSPSPGKCCSACSREST 416

Qy 267 TETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISA 326

Db 417 GFSYIC--SNKGCQDFLDV-----RCISVLEYFIHRSHEH-----PIFISTS 457

Qy 327 FATLFTVMCKKQENIYSHLDEESSE--SSTYTA--LPRE---RLRPRPKVFLCYSGSKOG 381

Db 458 YNSKDEILCKVKRCRCLGAHLQCLTCLCEFTWCYSCAIPDEIHYKFKDKHPLTSCGSAD- 516

Qy 382 QNHMNVVQCPAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMK 441

Db 517 ---NTWCEV-----CEKQDPKEWFTCNK---CCITIH-----LHCIFGSS 553

Qy 442 YFVDKKNYKHGGGRSGKGEFLVAVSAEAKLRQAKSSAALSKEFTAVYEDYSCEGD 501

Db 554 VFM-----KPG-----SIFRDYDKVQV 570

Qy 502 VPGILDLSLTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTROGSRN--YPRSKSGRSLY-V 558

Db 571 V-----FRNNSNTRQLCYMCHNRCTGL-----IPYEGYRNATYYNHSNRSTHRM 616

Qy 559 AICNM 563

Db 617 IFCSL 621

Search completed: August 9, 2005, 11:49:54

Job time : 35.2019 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:36:31 ; Search time 118.76 Seconds
(without alignments)
3246.847 Million cell updates/sec

Title: US-10-717-282-2
Perfect score: 4013
Sequence: 1 MAPWLQCSVFVTNACLING.....CKADLGCRSYDELHVAAPL 753

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3319	97.7	739	Q8NFS0	Q8nfs0 homo sapien
2	3315	97.6	739	Q8NFM7	Q8nfm7 homo sapien
3	3708	92.4	707	Q6RVF4	Q6rvf4 homo sapien
4	3703	92.3	728	Q6UW15	Q6uw15 homo sapien
5	3401.5	84.8	738	Q8JZL1	Q8jz11 mus musculus
6	3170	79.0	595	Q8N113	Q8n113 homo sapien
7	3005	74.9	564	Q9UFA0	Q9ufa0 homo sapien
8	2892	72.1	741	Q7T2L7	Q7t2l7 gallus gall
9	2834	70.6	697	Q8AV76	Q8av76 gallus gall
10	2675.5	66.7	594	Q8K447	Q8k447 mus musculus
11	2616.5	65.2	582	Q8R5J8	Q8r5j8 mus musculus
12	1961	48.9	745	Q8QHJ9	Q8qhj9 brachydanio
13	1952	48.6	745	Q8QHJ6	Q8qhj6 brachydanio
14	538	13.4	109	Q8HXE8	Q8hxe8 macaca fasc
15	310	7.7	866	117R_HUMAN	Q96f46 homo sapien
16	306	7.6	864	117R_MOUSE	Q60943 mus musculus
17	205	5.1	769	Q69HQ3	Q69hq3 ciona intes
18	170.5	4.2	846	Q9NA64	Q9na64 caenorhabdi
19	135.5	3.4	502	117S_HUMAN	Q9nmr6 homo sapien
20	126.5	3.2	718	YS02_CAEEL	Q10128 caenorhabdi
21	121	3.0	993	Q7PWU5	Q7pwu5 anopheles g
22	117.5	2.9	562	Q99755	Q99755 homo sapien
23	117	2.9	757	Q13399	Q13399 ustilago ma
24	117	2.9	917	Q81789	Q81789 arabidopsis
25	117	2.9	2946	Q64634	Q64634 arabidopsis
26	116.5	2.9	637	Q6AZ51	Q6az51 rattus norv
27	116.5	2.9	901	Q9KE04	Q9ke04 bacillus ha
28	116	2.9	4736	Q7YCY9	Q7ycy9 mytilus gal
29	115.5	2.9	938	Q60669	Q60669 mus musculus
30	115	2.9	859	MR1P_HUMAN	Q8ntw9 homo sapien
31	115	2.9	998	EPB3_HUMAN	P54753 homo sapien

32	113.5	2.8	617	2	Q8K4C1	Q8k4c1 mus musculus
33	113.5	2.8	1190	2	Q6H470	Q6h470 oryza sativ
34	112.5	2.8	549	2	Q99754	Q99754 homo sapien
35	112.5	2.8	783	2	Q6FJR3	Q6fjr3 candida gla
36	112.5	2.8	1685	2	Q6H969	Q6h969 homo sapien
37	112.5	2.8	1685	2	Q6ZU00	Q6zuu0 homo sapien
38	111.5	2.8	370	2	Q8N2R7	Q8n2r7 homo sapien
39	111.5	2.8	370	2	Q96KN9	Q96kn9 homo sapien
40	111.5	2.8	862	2	Q6NUR8	Q6nuk8 homo sapien
41	111	2.8	592	2	Q6C6D7	Q6c6d7 yarrowia li
42	111	2.8	1732	2	Q6ZQ20	Q6zq20 mus musculus
43	110.5	2.8	499	1	117S_MOUSE	Q91ip3 mus musculus
44	110.5	2.8	805	2	Q758M4	Q758m4 aethya goss
45	110.5	2.8	1433	2	Q6PFW1	Q6pfw1 homo sapien

ALIGNMENTS

RESULT 1
Q8NFS0 PRELIMINARY; PRT; 739 AA.
AC Q8NFS0;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE IL-17RD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbert J.M., Gorman D.M.;
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458067; AAM77571.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 739 AA; 82440 MW; 1670803DD0C0DF17 CRC64;

Query Match 97.7%; Score 3919; DB 2; Length 739;
Best Local Similarity 98.0%; Pred. NO. 2.2e-290;
Matches 738; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

QY	1	MAPWLQCSVFVTNACLINGSQLA	VAAGSGRARGADTCGWRMKAARPRLCVANEGVGP	60
DB	1	MAPWLQCSVFVTNACLINGSQLA	VAAGSGRARGADTCGWRMKAARPRLCVANEGVGP	46
QY	61	ASRNSGLYNTFKYDNCCTYLN	VPVKHVIADAQNITISQYACHDQVAVTILWSPGALGIE	120
DB	47	ASRNSGLYNTFKYDNCCTYLN	VPVKHVIADAQNITISQYACHDQVAVTILWSPGALGIE	106
QY	121	FLKGRFVILEELKSGROCOQIL	KDPQLNSSFRTGMSQPFLLMKFETDYFKVVPVF	180
DB	107	FLKGRFVILEELKSGROCOQIL	KDPQLNSSFRTGMSQPFLLMKFETDYFKVVPVF	166
QY	181	PSIKNESNYHFFPFRTRACD	LLQLPDNLACKPFWKPRNLINISQHGSDMQVSDHAPHNFG	240
DB	167	PSIKNESNYHFFPFRTRACD	LLQLPDNLACKPFWKPRNLINISQHGSDMQVSDHAPHNFG	226
QY	241	FRFFVLYHLKHGEPFKKTK	QEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA	300
DB	227	FRFFVLYHLKHGEPFKKTK	QEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA	286
QY	301	LKPVHSPWAGPIRAVAITV	PLVVISAFATLFTVMCRKQOENIYSHLDESESESTYTA	360
DB	287	LKPVHSPWAGPIRAVAITV	PLVVISAFATLFTVMCRKQOENIYSHLDESESESTYTA	346
QY	361	LPRELRPRPKVFLCYSSK	DGNHNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE	420
DB	347	LPRELRPRPKVFLCYSSK	DGNHNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE	406

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QY 421 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRSGKGEFLFVAVSAIAEKLRQAK 480
DB 407 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRSGKGEFLFVAVSAIAEKLRQAK 466
QY 481 SSSAALSFIAYFDYSCGDPVGLDLSKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 540
DB 467 SSSAALSFIAYFDYSCGDPVGLDLSKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 526
QY 541 QGSRNRYFRSKGSLYVAICNMHQFIDEBPDWFEKQFVPPHPPPLRYRREPVLEKPSGL 600
DB 527 QGSRNRYFRSKGSLYVAICNMHQFIDEBPDWFEKQFVPPHPPPLRYRREPVLEKPSGL 586
QY 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARPALDGSAAQLPL 660
DB 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARPALDGSAAQLPL 646
QY 661 LHTKAGSPSDMPRDSGIYDSSVPSSELSPLMEGLSTDQTSLSLTSVSSSSGLGEE 720
DB 647 LHTKAGSPSDMPRDSGIYDSSVPSSELSPLMEGLSTDQTSLSLTSVSSSSGLGEE 706
QY 721 PPALPSKLLSSGCKADLGCRSYTDELHVAAPL 753
DB 707 PPALPSKLLSSGCKADLGCRSYTDELHVAAPL 739

RESULT 2
QBNFM7 PRELIMINARY; PRT; 739 AA.
AC Q8NFM7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 17 receptor-like protein long form.
GN Name=IL17RLM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "hSef inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
[2]
RN SEQUENCE FROM N.A.
RP Xiong S.Q., Huang G.R., Zhao O.H., Chen P.L., Rong Z.L., Ye X.Y.,
RA Chen Y., Liu L., Fu X.X., Chang Z.J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF494208; AAM74077.1; -.
DR Genew; HGNC:17616; IL17RD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
KW Receptor.
SQ SEQUENCE 739 AA; 82441 MW; BCDA2A95261B0277 CRC64;

Query Match 97.6%; Score 3915; DB 2; Length 739;
Best Local Similarity 97.9%; Pred. No. 4.5e-290;
Matches 737; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFTVNAACLSQSLVAAGSGRARGADTCGRWMAAARPLCVANEGVGP 60
DB 1 MAPWLQCSVFTVNAACLSQSLVAAGSGRARGADTCGRWMAAARPLCVANEGVGP 46
QY 61 ASRNSGLNITFKYDNCNTYLNPKVKHVIADAQNTITISQACHDOVAVTILWSPCALGIE 120
DB 47 ASRNSGLNITFKYDNCNTYLNPKVKHVIADAQNTITISQACHDOVAVTILWSPCALGIE 106
QY 121 FLKGFVRVLEELKSGRCQOOLIKDPQLNSSFKRTGMESQPLNMFETDVFVKVVPF 180
DB 121 FLKGFVRVLEELKSGRCQOOLIKDPQLNSSFKRTGMESQPLNMFETDVFVKVVPF 166
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DB 107 FLKGFVRVLEELKSGRCQOOLIKDPQLNSSFKRTGMESQPLNMFETDVFVKVVPF 166
QY 181 PSIKNESNYHPPFRTRACDILLQPDNLACKPFWKPRNTANISOHGSQDMQVSFDHAPNFG 240
DB 167 PSIKNESNYHPPFRTRACDILLQPDNLACKPFWKPRNTANISOHGSQDMQVSFDHAPNFG 226
QY 241 FRPFLYHLKHGEPFKRKCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
DB 227 FRPFLYHLKHGEPFKRKCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286
QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 360
DB 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 346
QY 361 LPRERLPRPKVFLCYSSKDGQNHMVVQCFAVFLQDFCGCEVALDLWEDFSLCREGORE 420
DB 347 LPRERLPRPKVFLCYSSKDGQNHMVVQCFAVFLQDFCGCEVALDLWEDFSLCREGORE 406
QY 421 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRSGKGEFLFVAVSAIAEKLRQAK 480
DB 407 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRSGKGEFLFVAVSAIAEKLRQAK 466
QY 481 SSSAALSFIAYFDYSCGDPVGLDLSKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 540
DB 467 SSSAALSFIAYFDYSCGDPVGLDLSKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 526
QY 541 QGSRNRYFRSKGSLYVAICNMHQFIDEBPDWFEKQFVPPHPPPLRYRREPVLEKPSGL 600
DB 527 QGSRNRYFRSKGSLYVAICNMHQFIDEBPDWFEKQFVPPHPPPLRYRREPVLEKPSGL 586
QY 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARPALDGSAAQLPL 660
DB 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARPALDGSAAQLPL 646
QY 661 LHTKAGSPSDMPRDSGIYDSSVPSSELSPLMEGLSTDQTSLSLTSVSSSSGLGEE 720
DB 647 LHTKAGSPSDMPRDSGIYDSSVPSSELSPLMEGLSTDQTSLSLTSVSSSSGLGEE 706
QY 721 PPALPSKLLSSGCKADLGCRSYTDELHVAAPL 753
DB 707 PPALPSKLLSSGCKADLGCRSYTDELHVAAPL 739

RESULT 3
Q6RVF4 PRELIMINARY; PRT; 707 AA.
AC Q6RVF4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SEF splice variant b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUES=Testes;
RX PubMed=14742870; DOI=10.1073/pnas.0307952100;
RA Preger E., Ziv I., Shabtay A., Sher I., Tsang M., Dawid I.B.,
RA Altuvia Y., Ron D.;
RT "Alternative splicing generates an isoform of the human Sef gene with
RT altered subcellular localization and specificity.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:1229-1234(2004).
DR EMBL; AY489047; AAS15051.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 707 AA; 79493 MW; 7D3BE21EE038F17E CRC64;

Query Match 92.4%; Score 3708; DB 2; Length 707;
Best Local Similarity 99.7%; Pred. No. 2.8e-274;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 56 EGVGPASRNSGLYNTFKYDNCCTTLYLPVGVKHVIADQNITISQYACHDQVAVTILWSPG 115
RA :|||||
DB 10 QGVGPASRNSGLYNTFKYDNCCTTLYLPVGVKHVIADQNITISQYACHDQVAVTILWSPG 69
QY 116 ALGIEFLKGRFVILBELKSEGRQCOQILKDPKOLNSFKRTGMESQPFLLNMKPTDYFV 175
RA :|||||
DB 70 ALGIEFLKGRFVILBELKSEGRQCOQILKDPKOLNSFKRTGMESQPFLLNMKPTDYFV 129
QY 176 KVPFPPIKSNESYHPFFRTRACDILLOPNLACKPFWKPRNLNIHQSDMOVSFDHA 235
RA :|||||
DB 130 KVPFPPIKSNESYHPFFRTRACDILLOPNLACKPFWKPRNLNIHQSDMOVSFDHA 189
QY 236 PHNFGFFHYLYKLHEGPPKRTCKQEQTTETSCILQNVSPGDYIIEILDVDTNTRK 295
RA :|||||
DB 190 PHNFGFFHYLYKLHEGPPKRTCKQEQTTETSCILQNVSPGDYIIEILDVDTNTRK 249
QY 296 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKKQENIYSHLDESS 355
RA :|||||
DB 250 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKKQENIYSHLDESS 309
QY 356 TYTAALPRERLRPRPKVFLCYSSKXGQNMNVQCFAYFLQDFCGCEVALDLWEDFSLCR 415
RA :|||||
DB 310 TYTAALPRERLRPRPKVFLCYSSKXGQNMNVQCFAYFLQDFCGCEVALDLWEDFSLCR 369
QY 416 EGQREWIQKTHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGBELFLVAVSAIAEKL 475
RA :|||||
DB 370 EGQREWIQKTHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGBELFLVAVSAIAEKL 429
QY 476 RQAKQSSAALSFKTIAVYDYSCGDVPGILDLSTKYRLMDNLPLQCSHLHSRDHGLQEP 535
RA :|||||
DB 430 RQAKQSSAALSFKTIAVYDYSCGDVPGILDLSTKYRLMDNLPLQCSHLHSRDHGLQEP 489
QY 536 GQHTQSGRRNYFRSKSGRSYLVAINCMHQFIIDEEPWFEXQFVFPFPPPLRYREPVLK 595
RA :|||||
DB 490 GQHTQSGRRNYFRSKSGRSYLVAINCMHQFIIDEEPWFEXQFVFPFPPPLRYREPVLK 549
QY 596 FDSGLVLDVCMCKPESDFCLKVEAAVLGATGADSOHSGHGLDQDGEARPDGSA 655
RA :|||||
DB 550 FDSGLVLDVCMCKPESDFCLKVEAAVLGATGADSOHSGHGLDQDGEARPDGSA 609
QY 656 ALQPLLLHTVKAGSPDMPRDSGIVDSSVPSSSELSPLMEGLSTDQTTSSITSSVSSSG 715
RA :|||||
DB 610 ALQPLLLHTVKAGSPDMPRDSGIVDSSVPSSSELSPLMEGLSTDQTTSSITSSVSSSG 669
QY 716 LGEPEPPALPKLLSSGCKADLGRSYTDELHVAAPL 753
RA :|||||
DB 670 LGEPEPPALPKLLSSGCKADLGRSYTDELHVAAPL 707
RESULT 4
Q6UW15 PRELIMINARY; PRT; 728 AA.
ID Q6UW15;
AC Q6UW15;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE IL17Rhom.
DN ORFNames=UNQ6115;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowaki L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358774; AA089134.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 728 AA; 81310 MW; 4AD9D3F6B1C78C26 CRC64;
Query Match 92.3%; Score 3703; DB 2; Length 728;
Best Local Similarity 96.7%; Pred. No. 6.9e-274;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;
QY 42 RMKAARPRLCVANE-GVGPASRNSGLYNTFKYDNCCTTLYLPVGVKHVIADQNITISQY 100
DB 3 RASAGVPAALFVSGEQGVGPASRNSGLYNTFKYDNCCTTLYLPVGVKHVIADQNITISQY 62
QY 101 ACHDQVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQILKDPKOLNSFKRTGME 160
DB 63 ACHDQVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQILKDPKOLNSFKRTGME 122
QY 161 SQPPLNMKPTDYFVKKVVPFPPSKNESYHPFFRTRACDILLOPNLACKPFWKPRNLN 220
DB 123 SQPPLNMKPTDYFVKKVVPFPPSKNESYHPFFRTRACDILLOPNLACKPFWKPRNLN 182
QY 221 ISQ-----HGSDMOVSFDHAPHNFGFRFFLYLKLHEGPPKRTCKQEQTT 267
DB 183 ISQSGSDMOVSFDHAPHNFGFRFFLYLKLHEGPPKRTCKQEQTT 242
QY 268 ETTSCLLQNVSPGDYIIEILDVDTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 327
DB 243 EMTSCLLQNVSPGDYIIEILDVDTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 302
QY 328 ATLFVVMCKRKKQENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSKDQGNHNV 387
DB 303 ATLFVVMCKRKKQENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSKDQGNHNV 362
QY 388 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKX 447
DB 363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKX 422
QY 448 NYKHGGGSGKGBELFLVAVSAIAEKLRAQKSSAALSFKTIAVYDYSCGDVPGILD 507
DB 423 NYKHGGGSGKGBELFLVAVSAIAEKLRAQKSSAALSFKTIAVYDYSCGDVPGILD 482
QY 508 LSTKYRLMDNLPLQCSHLHSRDHGLQEPGQHTQSGRRNYFRSKSGRSYLVAINCMHQFI 567
DB 483 LSTKYRLMDNLPLQCSHLHSRDHGLQEPGQHTQSGRRNYFRSKSGRSYLVAINCMHQFI 542
QY 568 DEEPDWFEXQFVFPFPPPLRYREPVLKFDGLVLDVCMCKPESDFCLKVEAAVLGAT 627
DB 543 DEEPDWFEXQFVFPFPPPLRYREPVLKFDGLVLDVCMCKPESDFCLKVEAAVLGAT 602
QY 628 GPADSQHSQHGLDQDGEARPDGSAALQPLHTVKAGSPDMPRDSGIVDSSVPSSSE 687
DB 603 GPADSQHSQHGLDQDGEARPDGSAALQPLHTVKAGSPDMPRDSGIVDSSVPSSSE 662
QY 688 LSLPLMEGLSTDQTTSSITSSVSSSGGLGEEPPALPKLLSSGCKADLGRSYTDEL 747
DB 663 LSLPLMEGLSTDQTTSSITSSVSSSGGLGEEPPALPKLLSSGCKADLGRSYTDEL 722
QY 748 HAVAPL 753
DB 723 HAVAPL 728
RESULT 5
Q8JZL1 PRELIMINARY; PRT; 738 AA.
ID Q8JZL1
AC Q8JZL1;

Query Match 74.9%; Score 3005; DB 2; Length 564;
Best Local Similarity 99.8%; Pred. NO. 1e-220;
Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 190 HPEFFRTRACDLLLPDNLACKPFWKPNLNI SOGSDMQVSPDHPHNEGFFPFLYHK 249

Db 1 HPEFFRTRACDLLLPDNLACKPFWKPNLNI SOGSDMQVSPDHPHNEGFFPFLYHK 60

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RESULT 8
Q7T2L7 PRELIMINARY; PRT; 741 AA.
AC Q7T2L7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FGF signaling antagonist SEF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=42660508; PubMed=12766772; DOI=10.1038/ncb989;
RX Kawakami Y., Rodriguez-Leon J., Koth C.M., Buscher D., Itoh T.,
RA Raya A., Ng J.K., Rodriguez Esteban C., Takahashi S., Henrique D.,
RA Schwarz M.-F., Asahara H., Izpisua Belmonte J.C.;
RT "MKP3 mediates the cellular response to FGF8 signalling in the
RT vertebrate limb.";
RL Nat. Cell Biol. 5:513-519(2003).
RL EMBL; AY278204; AAP70001.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 741 AA; 83553 MW; 64B8E98241AC60CF CRC64;

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Query Match      72.1%; Score 2892; DB 2; Length 741;
Best Local Similarity 72.4%; Pred No. 6.e-212;
Matches 548; Conservative 79; Mismatches 110; Indels 20; Gaps 6

QY 1 MAPWLQLGSVEFTVNACLINGSOLAVAGGSGRARG--ADTCGRWRKAAARPLRCVANEV 58
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
DB 1 MAPGRELFALFALLAFCGSRRLFAEAGPGGRRGAADACGG-----GL 46
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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "Hsf inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
DR EMBL: AF494209; AAM74078.1; -.
DR MGI: 2159727; Il17rd.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR InterPro: IPR000157; TIR.
DR InterPro: IPR007087; Znf_C2H2.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 1.
KW Receptor.
SQ SEQUENCE 594 AA; 66780 MW; EABEG6B655DC4EC3 CRC64;

Query Match 66.7%; Score 2675.5; DB 2; Length 594;
Best Local Similarity 84.8%; Pred. No. 1.6e-195;
Matches 507; Conservative 34; Mismatches 50; Indels 7; Gaps 4;

QY 159 MESQFFLNKFKETDYFKVKKVPPPSIKNESNYHPPFFRTRACDLLQPNLACKPFWKPRN 218
DB 1 MESQFFLNKFKETDYFKVKKVPPPSIKNESNYHPPFFRTRACDLLQPNLACKPFWKPRN 60

QY 219 LNIHQSDMVOVSFDHAPHNFGFRFFYLHYKLKHEGPPFRKTKQEQTTTSCLLQNV 278
DB 1 LNIHQSDMVOVSFDHAPHNFGFRFFYLHYKLKHEGPPFRKTKQEQTTTSCLLQNV 120

QY 279 PGDYIIELVDNTNTRKVMHYALPKVSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 338
DB 1 PGDYIIELVDNTNTRKVMHYALPKVSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 180

QY 339 QOENIYSHLDESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVOCFAIFLQDF 398
DB 1 QOENIYSHLDESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVOCFAIFLQDF 240

QY 399 CGCEVALDLWDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRGS 458
DB 241 CGCEVALDLWDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRGS 300

QY 459 KGGEFLVAVSAIAEKLRQAKQSSAALSKFIATVFDYSCGDVPGIIDLSTKRLMDNL 518
DB 301 AQGEFFLVAVAAIAEKLRQAKQSSAALSKFIATVFDYSCGDVPGIIDLSTKRLMDNL 360

QY 519 POLCSHLHSRDHGLQEP-QOHTROGSRNNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQ 577
DB 361 PELCAHLHS---GEOEVLGQHPGHSSRRNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQ 417

QY 578 FVPHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATPADSOH--E 635
DB 418 FIPFQHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATPADSOH--E 477

QY 636 SQHGLDQDGEARPAIDGSAALQPLLTHTYKAGSPDMPDRSGIYDSSVPSSSELSLPLMEG 695
DB 478 SQHVLDDQTEAQPSCDSAPALQPLLTHTYKAGSPDMPDRSGIYDSSVPSSSELSLPLMEG 537

QY 696 LSTDTQTSSLTSSVSSSGLGEPPALPKLLSSGCKADLGCSTYDELHVAAPL 753
DB 538 LSPDQIETSSLTSSVSSSGLGEPPALPKLLSSGCKADLGCSTYDELHVAAPL 594

RESULT 11
Q8R5J8 ID Q8R5J8 PRELIMINARY; PRT; 582 AA.
AC Q8R5J8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Similar expression to FGF protein (Fragment).
GN Name=il17rd; Synonyms=Seif;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21824237; PubMed=11802165; DOI=10.1038/ncb750;
RA Furthauer M., Lin W., Ang S.L., Thiesse B., Thiesse C.;
RT "Seif is a feedback-induced antagonist of Ras/MAPK-mediated FGF
RT signaling.";
RL Nat. Cell Biol. 4:170-174(2002).
DR EMBL: AF424804; AAL79530.1; -.
DR MGI: 2159727; Il17rd.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR InterPro: IPR000157; TIR.
DR InterPro: IPR007087; Znf_C2H2.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 1.
FT NON_TER 1
SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 65.2%; Score 2616.5; DB 2; Length 582;
Best Local Similarity 84.6%; Pred. No. 5.1e-191;
Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;

QY 171 TDYFVKVVPFSPISKNESNYHPPFFRTRACDLLQPNLACKPFWKPRNLISQSDMHV 230
DB 1 TDYFVKVVPFSPISKNESNYHPPFFRTRACDLLQPNLACKPFWKPRNLISQSDMHV 60

QY 231 SFDHAPHNFGFRFFYLHYKLKHEGPPFRKTKQEQTTTSCLLQNVSPGYIIELVDNT 290
DB 61 SFDHAPHNFGFRFFYLHYKLKHEGPPFRKTKQEQTTTSCLLQNVSPGYIIELVDNT 120

QY 291 NTRKVMHYALPKVSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEE 350
DB 121 NTRKVMHYALPKVSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEE 180

QY 351 SSESSTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVOCFAIFLQDFCGCEVALDLWED 410
DB 181 SPESSTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVOCFAIFLQDFCGCEVALDLWED 240

QY 411 FSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGEAGQEFFLVAVSA 470
DB 241 FSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGEAGQEFFLVAVSA 300

QY 471 IAEKLRQAKQSSAALSKFIATVFDYSCGDVPGIIDLSTKRLMDNLPLCSHLHSRDH 530
DB 301 IAEKLRQAKQSSAALSKFIATVFDYSCGDVPGIIDLSTKRLMDNLPLCSHLHSRDH 357

QY 531 GLQEP-QOHTROGSRNNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQFVPHPPPLRYR 589
DB 358 GEOEVLGQHPGHSSRRNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQFVPHPPPLRYR 417

QY 590 EPTLEKFDGLVNDVMCKPGPESDFCLKVEAAVLGATPADSOH--ESQHGGLDQDGEA 647
DB 418 EPTLEKFDGLVNDVMCKPGPESDFCLKVEAAVLGATPADSOH--ESQHGGLDQDGEA 477

QY 648 RPALDGSAAQPLLAHTYKAGSPDMPDRSGIYDSSVPSSSELSLPLMEGLSDTQETSSLT 707
DB 478 QPSCDSPALQPLLAHTYKAGSPDMPDRSGIYDSSVPSSSELSLPLMEGLSDTQETSSLT 537

QY 708 ESVSSSSGLGEPPALPKLLSSGCKADLGCSTYDELHVAAPL 753
DB 538 ESVSSSSGLGEPPALPKLLSSGCKADLGCSTYDELHVAAPL 582

RESULT 12
Q8QHJ9
```


Db 464 SAIISEKLKEVHQSS-DLSRFMSVYFDYSHETDVTSLSLAPKFLMDQLPQLFARLHS 522

Qy 528 RDHGLQEPGQHTGSGRRNFRSRSGLSLVAICNMHQFIDEEDWPEKQFVPPHPPPLR 587

Db 523 RQLSLTREPQPPNVNKRNYFCSSGSLVAIYNMHQVTOEPDWLEKELM---PPPLP 579

Qy 588 YREPVLEKFGSLVINDVMCKPGSPESDFCLKVEAAVL-----GATGPADDSQHSQHGG 640

Db 580 NKRTIPEKVDGSLVNEVKLKHGSESE-CPVRSNVLLIPQTPGVGVSLSRDLDEGS 638

Qy 641 LDQGEARPALDGAALQPLHTVKAGSPSPDRSDGIYDSSVSSSELSPLMEGLSTDQ 700

Db 639 SSQD-----AGSCRPLVHTDGSAPPMPRDSGIYDSSVSSSELSPLMDGLSPDH 689

Qy 701 TETSLTESVSSSGLGEERPPALPSKLLSSGS-CKADL 738

Db 690 ADNSSLADSVSSSGLGDEEPPAVSSLHCTAHTICKADL 728

RESULT 14

Q8HXE8 PRELIMINARY; PRT; 109 AA.

AC Q8HXE8;

DT 01-MAR-2003 (TREMREL. 23, Created)

DT 01-MAR-2003 (TREMREL. 23, Last sequence update)

DT 01-MAR-2003 (TREMREL. 23, Last annotation update)

DE Hypothetical protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheinae; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Frontal lobe left;

RX MEDLINE=21459551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;

RA Osada N., Hida M., Kuehda J., Tanuma R., Iseki K., Hirata M., Suto Y.,

RA Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;

RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human

RT chromosomes.";

RL Gene 275:31-37(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Frontal lobe left;

RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB093642; BAC21616.1; -

KW Hypothetical protein.

QY SEQUENCE 109 AA; 11609 MW; 7EB13B49DB4C925B CRC64;

Query Match 13.4%; Score 538; DB 2; Length 109;

Best Local Similarity 87.2%; Pred. No. 2.9e-33;

Matches 102; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

Qy 1 MAPVLQCSVFTVNAVLGSLQSLAAGSGRARGADTCGRWKAARPRLCVANEGVGP 60

Db 1 MAPVLQCSVFTVNAVLGSLQSLAAGSGRARGADTCGRW-----GVGP 46

Qy 61 ASRNSGLNYITPKYDNTTYLNPVGHVIAADQNTISQYACHQDVAVTILMSPGAL 117

Db 47 ASRNSGLNYITPKYDNTTYLNPVGHVIAADQNTISQYACHQDVAVTILMSPGVL 103

RESULT 15

I17R HUMAN

ID Q96F46; O43844; PRT; 866 AA.

AC Q96F46; O43844;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Interleukin-17 receptor precursor (IL-17 receptor).

GN Name=IL17R;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=T-cell;

RX MEDLINE=98035683; PubMed=9367539; DOI=10.1006/cyto.1997.0240;

RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,

RA Vanden Bos T., Zappone J., Painter S.L., Armitage R.J.;

RT "Molecular characterization of the human interleukin (IL)-17

RT receptor.";

RL Cytokine 9:794-800(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.B.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP SEQUENCE OF 33-47.

RX PubMed=15340161; DOI=10.1110/ps.04682504;

RA Zhang Z., Henzel W.J.;

RT "Signal peptide prediction based on analysis of experimentally

RT verified cleavage sites.";

RL Protein Sci. 13:2819-2824(2004).

CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,

CC suggesting that additional components are involved in IL17-induced

CC signaling.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- TISSUE SPECIFICITY: Widely expressed.

CC -!- PTM: Glycosylated.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC or send an email to license@isb-sib.ch).

DR EMBL; U58917; AAB99730.1; -

DR EMBL; BC011624; AAH11624.1; -

DR Genbank; HGNC:5985; IL17R.

DR H-InvDB; HIX0016207; -

DR MIM; 605461; -

DR GO; GO:0005887; C: integral to plasma membrane; NAS.

DR GO; GO:0030368; F: interleukin-17 receptor activity; NAS.

DR GO; GO:0007166; P: cell surface receptor linked signal transdu. . ; NAS.

KW Direct protein sequencing; Glycoprotein; Receptor; Signal;

Transmembrane. 1 32

FT SIGNAL 33 866 Interleukin-17 receptor.

FT CHAIN 33 320 Extracellular (potential).

FT DOMAIN 321 341 Potential.

FT TRANSMEM 321 341

FT DOMAIN 342 866 Cytoplasmic (potential).

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:33:31 ; Search time 116.169 Seconds
(without alignments)
2390.439 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGRMKAAARPLCVAN.....CKADLGCRSYTDLHVAAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3829	100.0	753	5	ABB07626 Human cyt
2	3819	99.7	753	5	ABB07627 Human cyt
3	3741	97.7	739	5	ABB07628 Human cyt
4	3725	97.3	738	4	Aau09904 Human Int
5	3721	97.2	738	4	Aau09953 Human Int
6	3720	97.2	738	4	Aau09954 Human Int
7	3718	97.1	738	4	Aau09951 Human Int
8	3718	97.1	738	4	Aau09952 Human Int
9	3718	97.1	738	4	Aau09956 Human Int
10	3714	97.0	738	4	Aau09957 Human Int
11	3714	97.0	738	4	Aau09955 Human Int
12	3708	96.8	728	7	ADB65245 Human pro
13	3703	96.7	728	4	AAU04958 Human Int
14	3703	96.7	728	6	ABU89705 Human Int
15	3703	96.7	728	6	ABU72600 Human IL-
16	3703	96.7	728	6	ADA43241 Human Int
17	3703	96.7	728	7	ADA49782 Human Int
18	3703	96.7	728	7	ADA26975 Human PRO
19	3703	96.7	728	7	ADB66909 Human PRO
20	3703	96.7	728	7	ABW02061 Human IL-
21	3703	96.7	728	7	ADG87393 Human PRO
22	3703	96.7	728	7	ADL16689 Human PRO
23	3703	96.7	728	8	ADL16650 Human PRO
24	3703	96.7	728	8	ADL171310 Human IL-
25	3700	96.6	739	4	AAU10602 Human Int

ALIGNMENTS

RESULT 1

ABB07626

ID ABB07626 standard; protein; 753 AA.

XX ABB07626;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 amino acid sequence.

KW Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX N-PSDB; ABA95031, ABA95032.

XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.

XX Claim 1; Page 2; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumour growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which the
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial

26 3657.5 95.5 738 5 AAU11355
27 3208 83.8 739 5 ABB07630
28 3176 82.9 595 6 AAE33485
29 3170 82.8 595 4 ABUS3091
30 3166 82.7 595 5 ABP69026
31 2515.5 65.7 554 5 AAU91330
32 1334 34.6 236 4 AAU10601
33 312 8.1 866 2 AAU04185
34 312 8.1 866 2 AAU61272
35 312 8.1 866 2 AAU92409
36 312 8.1 866 3 AAU97131
37 312 8.1 866 3 AAU97181
38 312 8.1 866 3 AAB03807
39 312 8.1 866 3 AAU99941
40 312 8.1 866 4 AAB62066
41 312 8.1 866 4 AAU72754
42 312 8.1 866 5 ABB78079
43 312 8.1 866 7 ADD25546
44 312 8.1 866 8 ADJ88265
45 312 8.1 866 8 ADL24269

AAU11355 Human DNA
ABB07630 Murine cy
AAE33485 Human REM
ABUS3091 Human tra
ABP69026 Human pol
AAU91330 Human nov
AAU10601 5' portio
AAU04185 Human int
AAU61272 Human int
AAU92409 Human IL-
AAU97131 Human int
AAU97181 Human int
AAB03807 Human int
AAU99941 Human IL-
AAB62066 Human IL-
AAU72754 Human int
ABB78079 Amino aci
ADD25546 Binding d
ADJ88265 Human IL-
ADL24269 Human IL-

CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 amino acid sequence
XX
SQ Sequence 753 AA;
Query Match 100.0%; Score 3829; DB 5; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADTCGWRMKAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVKGHVIADAQNI 60
Db 36 ADTCGWRMKAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVKGHVIADAQNI 95
Qy 61 TISQYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSSFK 120
Db 96 TISQYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSSFK 155
Qy 121 RTGMESQPFLLNMKFETDYFKVVPFPSPISKNESNYHPFFRTRACDILLQDNLACKPFWK 180
Db 156 RTGMESQPFLLNMKFETDYFKVVPFPSPISKNESNYHPFFRTRACDILLQDNLACKPFWK 215
Qy 181 PRNLNISQHGSDMQVSPFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQ 240
Db 216 PRNLNISQHGSDMQVSPFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQ 275
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
Qy 301 RKQQENIYSHLDBESSESYTAAALPRERLRPRPKVFLCYSSKDGQGNHNMVQCFAYFL 360
Db 336 RKQQENIYSHLDBESSESYTAAALPRERLRPRPKVFLCYSSKDGQGNHNMVQCFAYFL 395
Qy 361 QDFCGCEVALDWMDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 420
Db 396 QDFCGCEVALDWMDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 455
Qy 421 RGSKGELFLVAVSAIAEKLRAQKSSAALSKEFIIVFYDSCRGDVPGLDLSKTYRLM 480
Db 456 RGSKGELFLVAVSAIAEKLRAQKSSAALSKEFIIVFYDSCRGDVPGLDLSKTYRLM 515
Qy 481 DNLPLQCSHLHSRDHGLQEPGQHTROGSRNRYFVSKGRSLYVAICNWHQFIDSEDPWEE 540
Db 516 DNLPLQCSHLHSRDHGLQEPGQHTROGSRNRYFVSKGRSLYVAICNWHQFIDSEDPWEE 575
Qy 541 KQFVFPFPPPLRYREPVLKEFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 600
Db 576 KQFVFPFPPPLRYREPVLKEFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 635
Qy 601 SQHGLDQDGEARPALDGSAAQLPLLHTVTKAGSPDMPRDSGIYDSSVPSSELSLPLMEG 660
Db 636 SQHGLDQDGEARPALDGSAAQLPLLHTVTKAGSPDMPRDSGIYDSSVPSSELSLPLMEG 695
Qy 661 LSTQDTETSSLTESVSSSGGEGEPPALPSKLLSSGCKADLCRSYTDDELHAVAPL 718
Db 696 LSTQDTETSSLTESVSSSGGEGEPPALPSKLLSSGCKADLCRSYTDDELHAVAPL 753
RESULT 2
ABB07627
ID ABB07627 standard; protein; 753 AA.
XX
AC ABB07627;
XX
XX
DT 20-MAY-2002 (first entry)
XX
XX Human cytokine receptor, Zcytor18 variant sequence.
DE
XX
KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 269 /label= T269M
FT /note= "wild-type Thr is replaced with Met"
FT Misc-difference 750 /label= V750A
FT /note= "wild-type Val is replaced with Ala"
XX
XX WO200208259-A2.
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US023253.
XX
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Presnell SR, Kuestner RE, Gao Z;
PI
XX WPI; 2002-217048/27.
DR N-PSDB; ABA95033, ABA95034.
XX
XX New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX
XX Disclosure; Page 94-98; 119pp; English.
XX
XX The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 variant amino acid sequence
XX
SQ Sequence 753 AA;
Query Match 99.7%; Score 3819; DB 5; Length 753;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ADTCGWRMKAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVKGHVIADAQNI 60
Db 36 ADTCGWRMKAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVKGHVIADAQNI 95
Qy 61 TISQYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSSFK 120
Db 96 TISQYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSSFK 155
Qy 121 RTGMESQPFLLNMKFETDYFKVVPFPSPISKNESNYHPFFRTRACDILLQDNLACKPFWK 180
Db 156 RTGMESQPFLLNMKFETDYFKVVPFPSPISKNESNYHPFFRTRACDILLQDNLACKPFWK 215
Qy 181 PRNLNISQHGSDMQVSPFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQ 240
Db 216 PRNLNISQHGSDMQVSPFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQ 275
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
Qy 301 RKQQENIYSHLDBESSESYTAAALPRERLRPRPKVFLCYSSKDGQGNHNMVQCFAYFL 360

Db 336 RKQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 395
Qy 361 QDFCGCEVALDLWEDFSLCRGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGG 420
Db 396 QDFCGCEVALDLWEDFSLCRGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGG 455
Qy 421 RSGKGBELFLVAVSAIAEKLQKQSSAALSKEFIAYVFDYSCGDPVGGILDSTKYRLM 480
Db 456 RSGKGBELFLVAVSAIAEKLQKQSSAALSKEFIAYVFDYSCGDPVGGILDSTKYRLM 515
Qy 481 DNLPLCSHLHSRDHGLQEPQCHTRQGSRRNRYFRSKGSRSLYVAICNMHQFIDEPDWFE 540
Db 516 DNLPLCSHLHSRDHGLQEPQCHTRQGSRRNRYFRSKGSRSLYVAICNMHQFIDEPDWFE 575
Qy 541 KQFVFPFPPPLRYREPVLKFDGSLVNDVMCKPSPESDFCLKVEAAVIGATGADSOHE 600
Db 576 KQFVFPFPPPLRYREPVLKFDGSLVNDVMCKPSPESDFCLKVEAAVIGATGADSOHE 635
Qy 601 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVSPSELSLPLMEG 660
Db 636 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVSPSELSLPLMEG 695
Qy 661 LSTDQTETSSITESVSSSGLGEPEPPALPSKLLSSGSKADLCGRSYTDELHAAVPL 718
Db 696 LSTDQTETSSITESVSSSGLGEPEPPALPSKLLSSGSKADLCGRSYTDELHAAVPL 753

RESULT 3
ABB07628 standard; protein; 739 AA.
XX ABB07628;
AC ABB07628;
XX 20-MAY-2002 (first entry)
DT Human cytokine receptor, Zcytor18 splice variant.
DE Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
XX Homo sapiens.
XX WO200208259-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-US023253.
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Kuestner RE, Gao Z;
XX WPI; 2002-217048/27.
XX N-PSDB; ABA95035, ABA95036.
XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
XX Claim 1; Page 102-106; 119pp; English.

CC The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are

CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 splice variant
XX
SQ Sequence 739 AA;
Query Match 97.7%; Score 3741; DB 5; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 704; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
Qy 1 ADTCGWRMKAARPRLCVANEVGPASRNSGLNITFKYDNCITTYLNPVGHVIAQAQNI 60
Db 36 ADTCGWR-----GVGPASRNSGLNITFKYDNCITTYLNPVGHVIAQAQNI 81
Qy 61 TISQYACHDQVAVTILWSPGALGIEFLKGRFVLEELKSEGRQCOQLILKDPKOLNSFK 120
Db 82 TISQYACHDQVAVTILWSPGALGIEFLKGRFVLEELKSEGRQCOQLILKDPKOLNSFK 141
Qy 121 RTGMESQPFLLNMKPFETDYFKVAVPFPFSIKNESNYHFFFRTRACDLLLQPDNLACKPFWK 180
Db 142 RTGMESQPFLLNMKPFETDYFKVAVPFPFSIKNESNYHFFFRTRACDLLLQPDNLACKPFWK 201
Qy 181 PRNLNISQHSQDMQVSFDHAPHNFGFRFFYLHYKLKHEGPPKRTCKQETETTSCLLQ 240
Db 202 PRNLNISQHSQDMQVSFDHAPHNFGFRFFYLHYKLKHEGPPKRTCKQETETTSCLLQ 261
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 262 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy 301 RKQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 360
Db 322 RKQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 381
Qy 361 QDFCGCEVALDLWEDFSLCRGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGG 420
Db 382 QDFCGCEVALDLWEDFSLCRGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGG 441
Qy 421 RSGKGBELFLVAVSAIAEKLQKQSSAALSKEFIAYVFDYSCGDPVGGILDSTKYRLM 480
Db 442 RSGKGBELFLVAVSAIAEKLQKQSSAALSKEFIAYVFDYSCGDPVGGILDSTKYRLM 501
Qy 481 DNLPLCSHLHSRDHGLQEPQCHTRQGSRRNRYFRSKGSRSLYVAICNMHQFIDEPDWFE 540
Db 502 DNLPLCSHLHSRDHGLQEPQCHTRQGSRRNRYFRSKGSRSLYVAICNMHQFIDEPDWFE 561
Qy 541 KQFVFPFPPPLRYREPVLKFDGSLVNDVMCKPSPESDFCLKVEAAVIGATGADSOHE 600
Db 562 KQFVFPFPPPLRYREPVLKFDGSLVNDVMCKPSPESDFCLKVEAAVIGATGADSOHE 621
Qy 601 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVSPSELSLPLMEG 660
Db 622 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVSPSELSLPLMEG 681
Qy 661 LSTDQTETSSITESVSSSGLGEPEPPALPSKLLSSGSKADLCGRSYTDELHAAVPL 718
Db 682 LSTDQTETSSITESVSSSGLGEPEPPALPSKLLSSGSKADLCGRSYTDELHAAVPL 739
RESULT 4
AAU09904 standard; protein; 738 AA.
XX AAU09904;
XX AC AAU09904;
XX 14-FEB-2002 (first entry)
XX Human Interleukin 17 (hIL-17) receptor like protein.
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytosolic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human.

Homo sapiens.

WO200168859-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-US008678.

16-MAR-2000; 2000US-0189816P.

28-NOV-2000; 2000US-00724460.

(AMGE-) AMGEN INC.

Jing S;

WPI; 2001-611392/70.

N-PSDB; AAS15346.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.

Claim 2; Page 152-154; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytosolic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantify the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human Interleukin 17 (IL-17) receptor like protein described in the method of the invention

Sequence 738 AA;

Query Match 97.3%; Score 3725; DB 4; Length 738;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

QY 2 DTCCGWMKAAARPRLCVANEGVGASRNSGLYNTTFKYDNCCTYLNPNVKGHVIAQAQNIIT 61

DB 37 DTCCGWR-----GVGASRNSGLYNTTFKYDNCCTYLNPNVKGHVIAQAQNIIT 82

QY 62 ISQYACHDQAVTILWSPGALGIFBLKGRFVILEELKSEGRQCQQLIKDPKQLNSSFKR 121

DB 83 ISQYACHDQAVTILWSPGALGIFBLKGRFVILEELKSEGRQCQQLIKDPKQLNSSFKR 142

QY 122 TGMESQPLNMKPTETDFYVKVPPSPSIKNESNYHPFFRTRACDILLQPNLACKPWP 181

DB 143 TGMESQPLNMKPTETDFYVKVPPSPSIKNESNYHPFFRTRACDILLQPNLACKPWP 202

QY 182 RNLNI SQHSDMQVSDPHAPNFGFRFFYLHYKLHKGHPFKRTCKQEQTTETSCILLQ 241

DB 203 RNLNISQHSDMQVSDPHAPNFGFRFFYLHYKLHKGHPFKRTCKQEQTTETSCILLQ 262

QY 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCR 301

DB 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVNCR 322

QY 302 KKOQENIYSHLDESSSESYTAALPRERLRPRPKVFLCYSSKDGQNHMVVOCFAFLQ 361

DB 323 KKOQENIYSHLDESSSESYTAALPRERLRPRPKVFLCYSSKDGQNHMVVOCFAFLQ 382

QY 362 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421

DB 383 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442

QY 422 GSGKGELFLVAVSAIAEKLRQAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGGR 481

DB 443 GSGKGELFLVAVSAIAEKLRQAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGGR 502

QY 482 NLPQLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNNHQFIDDEPDWFEK 541

DB 503 NLPQLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNNHQFIDDEPDWFEK 562

QY 542 QFVPPHPPPLRYREPVLKFDGLVLDNMVCKPESDFCLKVEAAVLGATGADSPADSHES 601

DB 563 QFVPPHPPPLRYREPVLKFDGLVLDNMVCKPESDFCLKVEAPVLGATGADSPADSHES 622

QY 602 QHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSELSLPLMEGL 661

DB 623 QHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSELSLPLMEGL 682

QY 662 STDQTTSSLTSSVSSSGSGEPEPPALPSKLLSSGCKADLCGRSYTDELHAPV 717

DB 683 STDQTTSSLTSSVSSSGSGEPEPPALPSKLLSSGCKADLCGRSYTDELHAPV 738

RESULT 5

AAU09953

ID AAU09953 standard; protein; 738 AA.

XX

AC AAU09953;

DT 14-FEB-2002 (first entry)

XX Human Interleukin 17 (hIL-17) receptor like protein substitution #3.

DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;

KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;

KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;

KW anti-leukaemic; anti-infertility; ophthalmological; lung disease;

KW bone disease; cancer; human; mutant;

KW mutein.

XX Homo sapiens.

OS Synthetic.

XX

FT Key Location/Qualifiers

FT Misc-difference 363 /label= Ser, Thr, Ala, Cys

FT

PN WO200168859-A2.

XX

PD 20-SEP-2001.

XX

PF 15-MAR-2001; 2001WO-US008678.

16-MAR-2000; 2000US-01899816P.
28-NOV-2000; 2000US-00724460.
(AMGE-) AMGEN INC.
Jing S;
WPI; 2001-611392/70.
Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
Claim 20; Page; 158pp; English.
The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-leukaemic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 20

Sequence 738 AA;
Query Match 97.2%; Score 3721; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

2 DTGWRKMAARPRLCVANEVGPASRNSGLYNTFKYDNCCTYLNPKVGHVADAQNI 61
|||||
37 DTGWR-----GVGPASRNSGLYNTFKYDNCCTYLNPKVGHVADAQNI 82
|||||
62 ISOYACHDQAVATILMSPGALGTEFLKGRVILEELKSGROCOQLILDKPKQLNSSPK 121
|||||
83 ISOYACHDQAVATILMSPGALGTEFLKGRVILEELKSGROCOQLILDKPKQLNSSPK 142
|||||
122 TGMESQFLNMKFETDYFVKVVPFPSPKSNESYHPFFFRTRACDLLQPDNLACKFPWKP 181
|||||
143 TGMESQFLNMKFETDYFVKVVPFPSPKSNESYHPFFFRTRACDLLQPDNLACKFPWKP 202
|||||
182 RNLNISQSGSDMQVDFHAPHNFGPRFFYLHYKLKHEGPFKTKCKEQTTFSTCLLQN 241
|||||
203 RNLNISQSGSDMQVDFHAPHNFGPRFFYLHYKLKHEGPFKTKCKEQTTFSTCLLQN 262
|||||
242 VSPGDYIIELVDDTNTTRKVMHYALKVPSPWAGPIRAVAITVPIVVISAFATLFTVMCR 301
|||||
263 VSPGDYIIELVDDTNTTRKVMHYALKVPSPWAGPIRAVAITVPIVVISAFATLFTVMCR 322
|||||
302 KKOENYSHLDESSSESTYTAALPRRLRPRKPVFLCYXSKGQNHMMVVQCFAFLQ 361
|||||

Db 323 KKOENYSHLDESSSESTYTAALPRRLRPRKPVFLCYXSKGQNHMMVVQCFAFLQ 381
Qy 362 DFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKQYKHKGGGR 421
Db 383 DFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKQYKHKGGGR 442
Qy 422 GSKGGLFLVAVSATAEKLROAKQSSAALSXPIAVYFDYSCGDPVPGILDLSLTKYRLMD 481
Db 443 GSKGGLFLVAVSATAEKLROAKQSSAALSXPIAVYFDYSCGDPVPGILDLSLTKYRLMD 502
Qy 482 NLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEDPWFEK 541
Db 503 NLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEDPWFEK 562
Qy 542 QFVPPHPPPLRYREPVLKEDFSLVNDVMCKPGPESDFCLKVEAAVLGATGPADSOHES 601
Db 563 QFVPPHPPPLRYREPVLKEDFSLVNDVMCKPGPESDFCLKVEAAVLGATGPADSOHES 622
Qy 602 QHGGILDODGEARPDGSAALQPLHLYKAGSPDMPRDSGIYDSSVSSLSLPLMEGL 661
Db 623 QHGGILDODGEARPDGSAALQPLHLYKAGSPDMPRDSGIYDSSVSSLSLPLMEGL 682
Qy 662 STQDTTSSLTSSVSSSGLGEEPPALPSKLLSSGCKADJGCRSYTDELHVAAP 717
Db 683 STQDTTSSLTSSVSSSGLGEEPPALPSKLLSSGCKADJGCRSYTDELHVAAP 738

RESULT 6
AAU09954
ID AAU09954 standard; protein; 738 AA.
XX AAU09954;
AC AAU09954;
XX 14-FEB-2002 (first entry)
DT Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
XX vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;
XX mutein.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 374
XX /label= Val, Ile, Met, Leu, Phe, Ala, Nle
XX WO200168859-A2.
XX 20-SEP-2001.
XX 15-MAR-2001; 2001WO-US008678.
XX 16-MAR-2000; 2000US-01899816P.
XX 28-NOV-2000; 2000US-00724460.
XX (AMGE-) AMGEN INC.
XX Jing S;
XX WPI; 2001-611392/70.
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
XX


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PS Claim 21; Page; 158pp; English.
XX
CC The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC anti-parkinsonian, anti-convulsant, anti-aesthetic, dermatological,
CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
CC ophthalmological activities. The IL-17 receptor like nucleic acids and
CC proteins may be used to prevent and treat diseases associated with
CC inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicaemia),
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human Interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 21
XX
SQ Sequence 738 AA;
Query Match 97.2%; Score 3720; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;
QY 2 DTCGWRKMAARPLCVANEGGVGSPASRNSGLYNTFKYDNCNTTYLNPVGKHIADAQNIT 61
DB |||||
37 DTCGWR-----GVGSPASRNSGLYNTFKYDNCNTTYLNPVGKHIADAQNIT 82
QY 62 ISQACHDOVAVTILSPGALGIEFLGFRVILEELSEGRQCOOLILKOPKQLNSSFKR 121
DB |||||
83 ISQACHDOVAVTILSPGALGIEFLGFRVILEELSEGRQCOOLILKOPKQLNSSFKR 142
QY 122 TGMESQPFLLNKFETDYFKVVPVPPSIKNESYHPPFFRTRACDLLLQPDNLACKPFWKP 181
DB |||||
143 TGMESQPFLLNKFETDYFKVVPVPPSIKNESYHPPFFRTRACDLLLQPDNLACKPFWKP 202
QY 182 RNLNISQHSQDMQVSFDHAPNFGFRFPYLHYKLKHEGPPFKRKTCKQEQTTTSCLLQN 241
DB |||||
203 RNLNISQHSQDMQVSFDHAPNFGFRFPYLHYKLKHEGPPFKRKTCKQEQTTTSCLLQN 262
QY 242 VSPGDYIIELVDDTNTTRKNVHYALKPVHSPWAGPIRAVAITPLVWISAFATLPTWCCR 301
DB |||||
263 VSPGDYIIELVDDTNTTRKNVHYALKPVHSPWAGPIRAVAITPLVWISAFATLPTWCCR 322
QY 302 KQQENIYSHLDESSSSTYTAALPRERLPRPKRVFLCYSSKDGQNHMNVVQCFAFLQ 361
DB |||||
323 KQQENIYSHLDESSSSTYTAALPRERLPRPKRVFLCYSSKDGQNHMNVVQCFAFLQ 382
QY 362 DFCGCEVALDWEFSLCREGQRBWVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
DB |||||
383 DFCGCEVALDWEFSLCREGQRBWVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
QY 422 GSGGGEFLVAVSAIAEKLRAKQSSAALSKEFTAVVFDYCEGDVPGILDLSKYRLMD 481
DB |||||
443 GSGGGEFLVAVSAIAEKLRAKQSSAALSKEFTAVVFDYCEGDVPGILDLSKYRLMD 502
QY 482 NLPQLCSHLHSDHGLQPGQHTTQGSRRNFRSKSGRSLVAICNMHQFIDEFPDWFKEK 541
DB |||||
503 NLPQLCSHLHSDHGLQPGQHTTQGSRRNFRSKSGRSLVAICNMHQFIDEFPDWFKEK 562
```

dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and and DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 18		Sequence 738 AA;	
CC	Query Match	97.18;	Score 3718; DB 4; Length 738;
CC	Best Local Similarity	97.68;	Pred. No. 0;
CC	Matches 699; Conservative	1;	Mismatches 2; Indels 14; Gaps 1;
Qy	2	DTCGWRKAAARPLRCVANEVGPASRNSGLYNTFKYDNCCTYLNFGVGHVIAQAQNIIT	61
Db	37	DTCGWR-----GVXPSRNSGLYNTFKYDNCCTYLNFGVGHVIAQAQNIIT	82
Qy	62	ISOYACHDQAVATILWSPGALGIEFLKGRFVILBELKSEGRQCOOLILKDPKLNSSFKR	121
Db	83	ISOYACHDQAVATILWSPGALGIEFLKGRFVILBELKSEGRQCOOLILKDPKLNSSFKR	142
Qy	122	TGMESQPLNKKFTDFVKVVPSPISKNSYHFFRFRACDLILQPNLACKPFWKP	181
Db	143	TGMESQPLNKKFTDFVKVVPSPISKNSYHFFRFRACDLILQPNLACKPFWKP	202
Qy	182	RNLNISQSGDMQVSDFAHNFGRFRFYHLKHEGPFKRTCKQEQTTTSCILQN	241
Db	203	RNLNISQSGDMQVSDFAHNFGRFRFYHLKHEGPFKRTCKQEQTTTSCILQN	262
Qy	242	VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAPATLFTWCR	301
Db	263	VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAPATLFTWCR	322
Qy	302	KKQENIYSHLDESSSSSTYTAALPRRLRPRKPVFLCYSSKDGQNHMNVVQCFAYFLQ	361
Db	323	KKQENIYSHLDESSSSSTYTAALPRRLRPRKPVFLCYSSKDGQNHMNVVQCFAYFLQ	382
Qy	362	DFCGCEVALDLWEDFSLCREGQREWVIOKHESQFIIVCCKGMKYFVCKKXKHKGGGR	421
Db	383	DFCGCEVALDLWEDFSLCREGQREWVIOKHESQFIIVCCKGMKYFVCKKXKHKGGGR	442
Qy	422	GSGKGLFLVAVSAIAEKLRAKQSSSAALSKFIAVFDYCEGDPGILDLSTKYRIMD	481
Db	443	GSGKGLFLVAVSAIAEKLRAKQSSSAALSKFIAVFDYCEGDPGILDLSTKYRIMD	502
Qy	482	NLPQCSHLHSDRHGLQBPQHTQGRSRNFRSKGSRSLVAICNMHQFTDEPDPFEK	541
Db	503	NLPQCSHLHSDRHGLQBPQHTQGRSRNFRSKGSRSLVAICNMHQFTDEPDPFEK	562
Qy	542	QFVFPHPPLRYRPLEVKFSGVLVNDVMCKPGPESDFCLKVRAVLGATGPADSDQES	601
Db	563	QFVFPHPPLRYRPLEVKFSGVLVNDVMCKPGPESDFCLKVRAVLGATGPADSDQES	622
Qy	602	QHGLDQGEARPALDGAALQPLILHTVKAGSPSDMPRDSGIYDSSVPSSELPLMEGL	661
Db	623	QHGLDQGEARPALDGAALQPLILHTVKAGSPSDMPRDSGIYDSSVPSSELPLMEGL	682
Qy	662	STDQTSSLTSSVSSSSGLGEEPPALPSKLLSGSGCKADLGCRSYTDELHAVAP	717
Db	683	STDQTSSLTSSVSSSSGLGEEPPALPSKLLSGSGCKADLGCRSYTDELHAVAP	738

RESULT 8	AAU09952	AAU09952 standard; protein; 738 AA.
ID	AAU09952	
XX	XX	
AC	AAU09952;	
XX	14-FEB-2002	(first entry)
DT	Human Interleukin 17 (hIL-17) receptor like protein substitution #2.	
DE	Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; mutein.	
XX	Homo sapiens.	
OS	Synthetic.	
XX	XX	
FX	Key	Location/Qualifiers
FT	Misc-difference 227	/label= Phe, Leu, Val, Ile, Ala, Tyr
FT	XX	
XX	XX	
PN	WO200168859-A2.	
XX	20-SEP-2001.	
XX	15-MAR-2001; 2001WO-US008678.	
XX	16-MAR-2000; 2000US-0189816P.	
PR	28-NOV-2000; 2000US-00724460.	
XX	(AMGE-) AMGEN INC.	
PA	Jing S;	
XX	WPI; 2001-611392/70.	
XX	Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.	
PS	Claim 19; Page; 158pp; English.	
XX	The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the	

CC	specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 19	XX
CC	Sequence 738 AA;	
CC	Query Match	
CC	Best Local Similarity 97.1%; Score 3718; DB 4; Length 738;	
CC	Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;	
QY	2 DTCGWRMKAARPRCLCVANGVGSPASNSGLYNTTPKYDNCCTTVLNPVGKHVIADAQNIIT 61	
DB	37 DTCGWR-----GVGPASNSGLYNTTFKYDNCCTTVLNPVGKHVIADAQNIIT 82	
QY	62 ISOYACHDQVAVTILMSPGALGTFIEFLKGFVRVILEELKSEGRQCOOLILKDPKOLNSSFKR 121	
DB	83 ISOYACHDQVAVTILMSPGALGTFIEFLKGFVRVILEELKSEGRQCOOLILKDPKOLNSSFKR 142	
QY	122 TGMESQPLANKPETDYFVKVPPPSIKNESNYHFFPTRACDLLLQPDNLACKPFWKP 181	
DB	143 TGMESQPLANKPETDYFVKVPPPSIKNESNYHFFPTRACDLLLQPDNLACKPFWKP 202	
QY	182 RNLNISQSGDMQVSPHAPNFGFRFFYLHYLKHGPPFKRCKQEQTTETTSCLLQN 241	
DB	203 RNLNISQSGDMQVSPHAPNFGFRFFYLHYLKHGPPFKRCKQEQTTETTSCLLQN 262	
QY	242 VSPGDYIIELVDDTNTTRKVMHYALKVHSPWAGPIRAVALTVPLVVISAFATLFTVMCR 301	
DB	263 VSPGDYIIELVDDTNTTRKVMHYALKVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322	
QY	302 KKOQENYSHLDESSSSTYTAALPRERLRPRPKVFLCYSSKDGQNMVMVQCFAFLQ 361	
DB	323 KKOQENYSHLDESSSSTYTAALPRERLRPRPKVFLCYSSKDGQNMVMVQCFAFLQ 382	
QY	362 DFCGCEVALDLWEDFSLCREGQREWWIQTTHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421	
DB	383 DFCGCEVALDLWEDFSLCREGQREWWIQTTHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442	
QY	422 GSGKGELFLVAVSAIAEKLQAKOSSAAALSKTATVTFDYSCGDVPGIILDLSTKYRLMD 481	
DB	443 GSGKGELFLVAVSAIAEKLQAKOSSAAALSKTATVTFDYSCGDVPGIILDLSTKYRLMD 502	
QY	482 NLPOLCSHLHSRDHGLQEPGQHTFRQSGRRNYFRSKSGRSLVYACNWHQFTIDEEPDMFEK 541	
DB	503 NLPOLCSHLHSRDHGLQEPGQHTFRQSGRRNYFRSKSGRSLVYACNWHQFTIDEEPDMFEK 562	
QY	542 QFVPFHPPLRYREPVLIEKFDGSLVLDVNMCKPESDFCLKVEAAVLGATGPADSQHS 601	
DB	563 QFVPFHPPLRYREPVLIEKFDGSLVLDVNMCKPESDFCLKVEAPVLGATGPADSQHS 622	
QY	602 QHGSLDQDGEARPALDGSAAALQPLLHTVTKAGSPSDMPRDSGIYDSSVPSSSELSLPLMEGL 661	
DB	623 QHGSLDQDGEARPALDGSAAALQPLLHTVTKAGSPSDMPRDSGIYDSSVPSSSELSLPLMEGL 682	
QY	662 STDQTETSSLTESVSSSGLGEPEPPALPSKLLSSGCKADLGRSYTDELHAVAP 717	
DB	683 STDQTETSSLTESVSSSGLGEPEPPALPSKLLSSGCKADLGRSYTDELHAVAP 738	
RESULT 9	AAU09956	
ID	AAU09956 standard; protein; 738 AA.	

KW	vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW	hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW	bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW	mutin.
OS	Homo sapiens.
OS	Synthetic.
OS	
FH	Key Location/Qualifiers
FT	Misc-difference 515
FT	/label= Asp, Glu
FT	
PN	WO200168859-A2.
PD	
PD	20-SEP-2001.
XX	
XX	15-MAR-2001; 2001WO-US008678.
PR	16-MAR-2000; 2000US-0189816P.
PR	28-NOV-2000; 2000US-00724460.
XX	
XX	(AMGE-) AMGEN INC.
PA	
PI	Jing S;
PI	
XX	
DR	WPI; 2001-611392/70.
XX	
PT	Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT	for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT	psoriasis and glaucoma.
XX	
PS	Claim 23; Page; 158pp; English.
XX	
XX	The invention describes novel nucleic acids encoding interleukin (IL) 17
CC	receptor like polypeptides useful as vaccines and in gene therapy. These
CC	have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC	immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC	anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC	osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
CC	ophthalmological activities. The IL-17 receptor like nucleic acids and
CC	proteins may be used to prevent and treat diseases associated with
CC	inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC	include, for example immune disorders (e.g. inflammation, diabetes and
CC	transplant rejection), infections (e.g. hepatitis and septicemia),
CC	weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC	dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC	lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin diseases
CC	(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC	bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC	(e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
CC	breast cancer), reproductive disorders (e.g. infertility and
CC	miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC	DNA and its complements may also be used as diagnostic probes to detect and
CC	quantitate the presence of similar nucleic acids in samples and identify
CC	patients needing restorative therapy. The IL17rlp may also be used as
CC	antigens in the production of antibodies against the proteins and in
CC	assays to identify modulators of expression and activity. The anti-
CC	IL17rlp antibodies and antagonists may also be used to down regulate
CC	expression and activity. Note: This sequence is not given in the
CC	specification but is based on the human interleukin 17 (IL-17) receptor
CC	like protein sequence (AAU09904) and has been created according to
CC	information given in claim 23
CC	

[illegible]

QY 62 ISOVACHDOVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQLILKDPKQLNSFFKR 121
DB 83 ISOVACHDOVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQLILKDPKQLNSFFKR 142
QY 122 TGMESQPLNKKFTDYFVKVVPFSPKSNESNYHPFFRTRACDLILLOPNLACKPFWKP 181
DB 143 TGMESQPLNKKFTDYFVKVVPFSPKSNESNYHPFFRTRACDLILLOPNLACKPFWKP 202
QY 182 RNLNISQHSQDMQVSDHAPHNFGFRFFYLHYKLKHEGPPKRTCKOBQTETTSCLLQN 241
DB 203 RNLNISQHSQDMQVSDHAPHNFGFRFFYLHYKLKHEGPPKRTCKOBQTETTSCLLQN 262
QY 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 301
DB 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 322
QY 302 KKOQENYSHLDRESSSSTVTAALPRELRPRPKVFLCYSSKDGQGNHNVVQCFAYFLQ 361
DB 323 KKOQENYSHLDRESSSSTVTAALPRELRPRPKVFLCYSSKDGQGNHNVVQCFAYFLQ 382
QY 362 DFCCEVALDLWEDFSLCREGQEWVIOKHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
DB 383 DFCCEVALDLWEDFSLCREGQEWVIOKHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
QY 422 GSGKGLFLVAVSAIAEKLRQAKOSSAALSKFTAVFDYSCGDVPGILDSTKYRLMD 481
DB 443 GSGKGLFLVAVSAIAEKLRQAKOSSAALSKFTAVFDYSCGDVPGILDSTKYRLMD 502
QY 482 NLPQLCSHLHRDGLQPGQHTQGRNRYFRSKSGRSLYVAICNMHQFIDEPPDWFPEK 541
DB 503 NLPQLCSHLHRDGLQPGQHTQGRNRYFRSKSGRSLYVAICNMHQFIDEPPDWFPEK 562
QY 542 QFVFPHPPLRYRBPVLEKPSGLVNDVMCKPGPESDFCLKVEAVLGATGCPADSOHES 601
DB 563 QFVFPHPPLRYRBPVLEKPSGLVNDVMCKPGPESDFCLKVEAVLGATGCPADSOHES 622
QY 602 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPDRDSGIYDSSVPSSLSLPLMEGL 661
DB 623 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPDRDSGIYDSSVPSSLSLPLMEGL 682
QY 662 STDQTSSTLSESVSSSGLEGEPPALPFSKLLSGSCADLGCRTSYTDELHAVAP 717
DB 683 STDQTSSTLSESVSSSGLEGEPPALPFSKLLSGSCADLGCRTSYTDELHAVAP 738

RESULT 10
AAU09957
ID AAU09957 standard; protein; 738 AA.
XX AC AAU09957;
XX DT 14-FEB-2002 (first entry)
XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

XX DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutein.
XX KW Homo sapiens.
OS OS Synthetic.
XX XX
FH Key Location/Qualifiers
FT Misc-difference 602
FT /label= Cys, Ala, Ser
XX PN
XX WO200168859-A2.

PD 20-SEP-2001.
XX 15-MAR-2001; 2001WO-US008678.
XX 16-MAR-2000; 2000US-0189816P.
PR 28-NOV-2000; 2000US-00724460.
XX (AMGE-) AMGEN INC.
XX Jing S;
XX WPI; 2001-611392/70.
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT psoriasis and glaucoma.
XX Claim 24; Page; 158pp; English.
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
CC ophthalmological activities. The IL-17 receptor like nucleic acids and
CC proteins may be used to prevent and treat diseases associated with
CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicemia),
CC weight disorders (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC dysfunction (e.g. Alzheimers disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone disease (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human Interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 24
XX SQ Sequence 738 AA;

Query Match 97.0%; Score 3714; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;
QY 2 DTCGWRKAAARPLCVANEGVGPASRNSGLYNTFFKYDNCNTTYLNPVGKHVIAQAQNT 61
DB 37 DTCGWR-----GVGPASRNSGLYNTFFKYDNCNTTYLNPVGKHVIAQAQNT 82
QY 62 ISOVACHDOVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQLILKDPKQLNSFFKR 121
DB 83 ISOVACHDOVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQLILKDPKQLNSFFKR 142
QY 122 TGMESQPLNKKFTDYFVKVVPFSPKSNESNYHPFFRTRACDLILLOPNLACKPFWKP 181
DB 143 TGMESQPLNKKFTDYFVKVVPFSPKSNESNYHPFFRTRACDLILLOPNLACKPFWKP 202
QY 182 RNLNISQHSQDMQVSDHAPHNFGFRFFYLHYKLKHEGPPKRTCKOBQTETTSCLLQN 241
DB 203 RNLNISQHSQDMQVSDHAPHNFGFRFFYLHYKLKHEGPPKRTCKOBQTETTSCLLQN 262
QY 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 301

Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322
Qy 302 KKOENIYSHLDDESSSTYTAALPRERLRPRKPVFLCYSSKDGQNHMMNVQCFAYFLQ 361
Db 323 KKOENIYSHLDDESSSTYTAALPRERLRPRKPVFLCYSSKDGQNHMMNVQCFAYFLQ 382
Qy 362 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
Db 383 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
Qy 422 GSGKGELFLVAVSAIAEKLRQAKOSSAALSCKFTAVTFDYSCGDVPGILDLSKYRLMD 481
Db 443 GSGKGELFLVAVSAIAEKLRQAKOSSAALSCKFTAVTFDYSCGDVPGILDLSKYRLMD 502
Qy 482 NLPOLCSHLHRDGLQEPGQHTQGGRRNFRSKSGRSLYVAICNWHQFTDESPDWFEK 541
Db 503 NLPOLCSHLHRDGLQEPGQHTQGGRRNFRSKSGRSLYVAICNWHQFTDESPDWFEK 562
Qy 542 QFVFPFPPPLYRYPVLEKFDGLVNDVMCKPGPESDFCLKVBAAVLGATGPAQSQHS 601
Db 563 QFVFPFPPPLYRYPVLEKFDGLVNDVMCKPGPESDFCLKVBAAVLGATGPAQSQHS 622
Qy 602 QHGLDQDGEARPALDGSAAALQPLLHTVYKAGSPDMPRDSGYDSSVPSSELSLPLMEGL 661
Db 623 QHGLDQDGEARPALDGSAAALQPLLHTVYKAGSPDMPRDSGYDSSVPSSELSLPLMEGL 682
Qy 662 STDQETSSLTSSVSSGLGEEPPALPSKLLSSGCKADLGCRSYTDLHVAAP 717
Db 683 STDQETSSLTSSVSSGLGEEPPALPSKLLSSGCKADLGCRSYTDLHVAAP 738

RESULT 11

AAU09955
ID AAU09955 standard; protein; 738 AA.
XX
AC AAU09955;
XX
DT 14-FEB-2002 (first entry)
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cycostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 385
FT /label= Cys, Ser, Ala
XX
XX WO200168859-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-US008678.
XX
XX 16-MAR-2000; 2000US-0189816P.
XX 28-NOV-2000; 2000US-00724460.
XX
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
XX
XX WPI; 2001-611392/70.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful

PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
XX
PT Claim 22; Page; 158pp; English.
XX
CC The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cycostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the CC specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to CC information given in claim 22
XX

Sequence 738 AA;

Query Match 97.0%; Score 3714; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;
Qy 2 DTCGRMKAARPLRCVANEVGPAGNSGLYNITFKYDNCCTTYLNPVGKHVIADAQNIT 61
Db 37 DTCGWR-----GVCPSGRNSGLYNITFKYDNCCTTYLNPVGKHVIADAQNIT 82
Qy 62 ISOYACHDQAVVILNWSGALGIEFLKPRVILEELKSEGRQCOQLILKDPKQLNSSFKR 121
Db 83 ISOYACHDQAVVILNWSGALGIEFLKPRVILEELKSEGRQCOQLILKDPKQLNSSFKR 142
Qy 122 TGMESQPLNMKFETDYFVKVVPFPSPISKNSNYHPFFRTRACDLILQPNLACKPFWKP 181
Db 143 TGMESQPLNMKFETDYFVKVVPFPSPISKNSNYHPFFRTRACDLILQPNLACKPFWKP 202
Qy 182 RNLNISQHGSDMQVSDHAPHNFGFRFFYLHYLKHGEPFKRKTCKOEQTETTSCLLQN 241
Db 203 RNLNISQHGSDMQVSDHAPHNFGFRFFYLHYLKHGEPFKRKTCKOEQTETTSCLLQN 262
Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 301
Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322
Qy 302 KKOENIYSHLDDESSSTYTAALPRERLRPRKPVFLCYSSKDGQNHMMNVQCFAYFLQ 361
Db 323 KKOENIYSHLDDESSSTYTAALPRERLRPRKPVFLCYSSKDGQNHMMNVQCFAYFLQ 382
Qy 362 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
Db 383 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
Qy 422 GSGKGELFLVAVSAIAEKLRQAKOSSAALSCKFTAVTFDYSCGDVPGILDLSKYRLMD 481
Db 443 GSGKGELFLVAVSAIAEKLRQAKOSSAALSCKFTAVTFDYSCGDVPGILDLSKYRLMD 502

Qy 482 NLPQLCSHLHSDHGLQPGQHTQGSRRNYFRSKSGSLYVAICNMHQFIDEPPDWFEX 541
Db 503 NLPQLCSHLHSDHGLQPGQHTQGSRRNYFRSKSGSLYVAICNMHQFIDEPPDWFEX 562
Qy 542 QFVFPHPPLRYRBPVLEKFDGSLVNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES 601
Db 563 QFVFPHPPLRYRBPVLEKFDGSLVNDVMCKPGPESDFCLKVEAPVLGATGPADSQHES 622
Qy 602 QHGGLDQGEARPALDGSAAALQPLLHTVVKAGSPSDMPRDSGIYDSSVPSSLSLPLMEGL 661
Db 623 QHGGLDQGEARPALDGSAAALQPLLHTVVKAGSPSDMPRDSGIYDSSVPSSLSLPLMEGL 682
Qy 662 STDQTSSLTSSVSSSSGLGEEPPALPSPKLLSSGSKADLGCRTSYDELHAVAP 717
Db 683 STDQTSSLTSSVSSSSGLGEEPPALPSPKLLSSGSKADLGCRTSYDELHAVAP 738

RESULT 12
ADB65245
ID ADB65245 standard; protein; 728 AA.
XX ADB65245;
AC ADB65245;
XX 04-DEC-2003 (first entry)
XX Human protein encoded by clone TESTI20046540.

XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX Homo sapiens.
XX EP1308459-A2.
XX 07-MAY-2003.
XX 28-MAR-2002; 2002EP-00007401.
XX 05-NOV-2001; 2001JP-00379298.
XX 25-JAN-2002; 2002US-00350978.
XX (HELI-) HELIX RES INST.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-450961/43.
DR N-PSDB; ADB63275.

XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX Claim 1; Page; 222pp; English.
XX The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets

CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX Sequence 728 AA;

Query Match 96.8%; Score 3708; DB 7; Length 728;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 21 EGVGPASRNSGLNITFKYDNCCTTLYNPVGHVADAGNITISQYACHDQAVATILWSPG 80
Db 31 QGVGPASRNSGLNITFKYDNCCTTLYNPVGHVADAGNITISQYACHDQAVATILWSPG 90
Qy 81 ALGIEFLKGRPVILEELKSEGRQCOQLILKDPKOLNSSFKRTGMSQPFLLNMKFTDYFV 140
Db 91 ALGIEFLKGRPVILEELKSEGRQCOQLILKDPKOLNSSFKRTGMSQPFLLNMKFTDYFV 150
Qy 141 KVPFPSPISKESNYHPFFRTRACDLLLLQPDNLACKPFWKPRNLNISQHSMDQVSPDHA 200
Db 151 KVPFPSPISKESNYHPFFRTRACDLLLLQPDNLACKPFWKPRNLNISQHSMDQVSPDHA 210
Qy 201 PHNFGFRFFYLHYKLKHEGPPKRTCKQEQTEITSCLLQNVSPGDYIIELVDDNTTRK 260
Db 211 PHNFGFRFFYLHYKLKHEGPPKRTCKQEQTEITSCLLQNVSPGDYIIELVDDNTTRK 270
Qy 261 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSS 320
Db 271 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSS 330
Qy 321 TYTAALPRERLRPRPKVFLCYSSKDGQNHMNVQCFAYFLQDFCCEVALDLWEDFSLCR 380
Db 331 TYTAALPRERLRPRPKVFLCYSSKDGQNHMNVQCFAYFLQDFCCEVALDLWEDFSLCR 390
Qy 381 EGQREWVIQTHESQFIIIVCSKGMKYFVDKKNYKHGSGGSGKGLFLVAVSAIAEKL 440
Db 391 EGQREWVIQTHESQFIIIVCSKGMKYFVDKKNYKHGSGGSGKGLFLVAVSAIAEKL 450
Qy 441 ROAKOSSAALSRTAVYFDYSCGDPVGIILDLSTKYRLMDNLPLCASHLHSDHGLQBP 500
Db 451 ROAKOSSAALSRTAVYFDYSCGDPVGIILDLSTKYRLMDNLPLCASHLHSDHGLQBP 510
Qy 501 QOHTROGSRNNYFRSKSGSLYVAICNMHQFIDEPPDWFEXQFVFPHPPLRYRBPVLEK 560
Db 511 QOHTROGSRNNYFRSKSGSLYVAICNMHQFIDEPPDWFEXQFVFPHPPLRYRBPVLEK 570
Qy 561 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQGEARPALDGS 620
Db 571 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQGEARPALDGS 630
Qy 621 ALQPLLHTVVKAGSPSDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSVSSSG 680
Db 631 ALQPLLHTVVKAGSPSDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSVSSSG 690
Qy 681 LGEHEPPALPSKLLSSGSKADLGCRTSYDELHAVAPL 718
Db 691 LGEHEPPALPSKLLSSGSKADLGCRTSYDELHAVAPL 728

RESULT 13
AAU04958
ID AAU04958 standard; protein; 728 AA.
XX AAU04958;
XX 24-OCT-2001 (first entry)

Db 423 NYKHGGGSGKGEFLVAVSAIAEKLRAQAKSSAALSXFIAYFYDYSCEGDPVPGILD 482
 Qy 473 LSTKYRLMDNLPQLCSHLHSDHGLQBPQHTROGSRNRYFRSKSGSLYVAICNMHQFI 532
 Db 483 LSTKYRLMDNLPQLCSHLHSDHGLQBPQHTROGSRNRYFRSKSGSLYVAICNMHQFI 542
 Qy 533 DEEDWFEKQVPFPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 592
 Db 543 DEEDWFEKQVPFPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 602
 Qy 593 GPADSOHSGUGGLDQDGEARPALDGSAAALPILHTYKAGSPDMPRDSGYDSSVPSSE 652
 Db 603 GPADSOHSGUGGLDQDGEARPALDGSAAALPILHTYKAGSPDMPRDSGYDSSVPSSE 662
 Qy 653 LSLPLMEGLSDQTETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDDEL 712
 Db 663 LSLPLMEGLSDQTETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDDEL 722
 Qy 713 HAVAPL 718
 Db 723 HAVAPL 728

RESULT 14
 ABU89705
 ID ABU89705 standard; protein; 728 AA.
 AC ABU89705;
 XX
 DT 10-JUL-2003 (first entry)
 XX
 DE Human interleukin 17 homologue PRO20026.
 XX
 KW Human; interleukin 17; IL-17; IL17 receptor; angiogenesis;
 KW T-lymphocyte proliferation; inflammatory cell infiltration;
 KW immune related disorder; systemic lupus erythematosus; osteoarthritis;
 KW rheumatoid arthritis; spondyloarthritis; systemic sclerosis;
 KW Sjogren's syndrome; sarcoidosis; autoimmune haemolytic anaemia;
 KW thyroiditis; diabetes mellitus; immune-mediated renal disease;
 KW demyelinating disease; Guillain-Barre syndrome; hepatobiliary disease;
 KW hepatitis; inflammatory bowel disease; Whipple's disease; psoriasis;
 KW immune-mediated skin disease; erythema multiforme; contact dermatitis;
 KW allergic disease; asthma; atopic dermatitis; food hypersensitivity;
 KW urticaria; immunologic disease of the lung; eosinophilic pneumonia;
 KW idiopathic pulmonary fibrosis; transplantation associated disease;
 KW graft-versus-host disease.
 XX
 OS Homo sapiens.
 XX
 PN US2003003546-A1.
 XX
 PD 02-JAN-2003.
 XX
 PF 22-MAR-2001; 2001US-00816744.
 XX
 PR 15-MAY-1998; 98US-0085579P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 21-APR-1999; 99US-0130232P.
 PR 26-APR-1999; 99US-0130222P.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99US-0134287P.
 PR 14-MAY-1999; 99WO-US010733.
 PR 09-JUN-1999; 99US-0138387P.
 PR 23-DEC-1999; 99US-0172096P.
 PR 30-DEC-1999; 99WO-US031274.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 02-JUN-2000; 2000WO-US015264.

PR 22-JUN-2000; 2000US-0213807P.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 24-OCT-2000; 2000US-0242837P.
 PR 26-OCT-2000; 2000US-0244072P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032878.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.

(GETH) GENENTECH INC.

Chen J, Filvaroff E, Fong S, Coddard A, Godowski P, Grimaldi C;
 Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandien R;
 Watanabe C, Williams PM, Wood WI, Yansura D;

WPI; 2003-428843/40.

N-FSDB; ACA89858.

New PRO polypeptides and polynucleotides homologous to interleukin-17,
 useful for treating e.g. systemic lupus erythematosus, rheumatoid
 arthritis, osteoarthritis, juvenile chronic arthritis, or systemic
 sclerosis.

Claim 10; Fig 18; 129pp; English.

The invention relates to a nucleic acid having similarity to interleukin-
 17 (IL-17) or IL-17 receptor comprises at least 80% nucleic acid sequence
 identity to a nucleotide sequence which: (a) encodes a polypeptide having
 a sequence of appearing as ABU89697-ABU89700 and ABU89702-ABU89705 (PI-
 p8), lacking or having its associated signal peptide; (b) encodes an
 extracellular domain of PI-p8 lacking its associated signal peptide; (c)
 consists of a sequence of appearing as ACA89850-ACA89853 and ACA89855-
 ACA8985867; or (d) consists of the full-length coding sequence of
 selected from SI-S8, and of the cDNA deposited under ATCC accession
 number 209866, 203522, PTA-1185, PTA-2108, PTA-202, PTA-1535, PTA-1082 or
 PTA-2591. Also included are expression vectors, host cells, encoded
 proteins, chimaeric proteins, antibodies, ant/agonists, compounds
 inhibiting the expression of SI-S8 or activity (or mimicking the activity
 of) of PI-p8, stimulating/inhibiting the proliferation of T-lymphocytes
 using the polypeptides or ant/agonists, enhancing the infiltration of
 inflammatory cells into a tissue of a mammal by administering a PRO1031
 polypeptide, its an agonist or antagonist, and inhibiting angiogenesis
 induced by a PRO1031 polypeptide or its agonist in a mammal by
 administering a PRO1031 polypeptide, its ant/agonist or an anti-PRO1031
 antibody. The proteins, antibodies, ant/agonists and compounds are useful
 for treating an immune related disorder such as systemic lupus
 erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
 arthritis, a spondyloarthritis, systemic sclerosis, an idiopathic
 inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
 thyroiditis, diabetes mellitus, immune-mediated renal disease, a
 demyelinating disease of the central or peripheral nervous system, a
 idiopathic demyelinating polynuropathy, Guillain-Barre syndrome, a
 chronic inflammatory demyelinating polynuropathy, a hepatobiliary
 disease, infectious or autoimmune chronic active hepatitis, primary
 biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 disease, an autoimmune or immune-mediated skin disease, a bullous skin
 disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 disease, asthma, allergic rhinitis, atopic dermatitis, food
 hypersensitivity, urticaria, an immunologic disease of the lung,
 eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 pneumonitis, a transplantation associated disease, graft rejection or
 graft-versus-host disease. The present sequence represents an IL17 or
 IL17 receptor homologue of the invention

Sequence 728 AA;

Query Match 96.7%; Score 3703; DB 6; Length 728;

Best Local Similarity 96.7%; Pred. No. 0;

Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:38:07 ; Search time 29.2862 Seconds
(without alignments)
1830.146 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGRWKAARPRLCVAN.....CKADLGCRSYTELHVAAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3703	96.7	728	4	US-09-747-259-18
2	3703	96.7	728	4	US-09-816-744-18
3	312	8.1	866	2	US-08-620-694A-10
4	312	8.1	866	3	US-09-022-255-10
5	312	8.1	866	3	US-09-022-696-10
6	312	8.1	866	3	US-08-978-773-4
7	312	8.1	866	3	US-09-022-253-10
8	312	8.1	866	3	US-09-022-260-10
9	312	8.1	866	3	US-09-022-259-10
10	312	8.1	866	3	US-09-022-257-10
11	312	8.1	866	4	US-09-549-679-10
12	312	8.1	866	4	US-10-033-522-1
13	306	8.0	864	2	US-08-620-694A-2
14	306	8.0	864	3	US-09-022-255-2
15	306	8.0	864	3	US-09-022-696-2
16	306	8.0	864	3	US-08-978-773-2
17	306	8.0	864	3	US-09-022-253-2
18	306	8.0	864	3	US-09-022-260-2
19	306	8.0	864	3	US-09-022-259-2
20	306	8.0	864	3	US-09-022-257-2
21	306	8.0	864	4	US-09-549-679-2
22	135.5	3.5	385	4	US-09-599-360B-106
23	135.5	3.5	502	4	US-09-747-259-12
24	135.5	3.5	502	4	US-09-816-744-12
25	135.5	3.5	504	4	US-09-949-016-11658
26	116	3.0	552	4	US-09-949-016-8005
27	113.5	3.0	617	3	US-09-188-930-303

28	113.5	3.0	617	4	US-09-312-283C-303
29	112.5	2.9	549	4	US-09-949-016-6384
30	111.5	2.9	489	4	US-09-248-796A-25826
31	110.5	2.9	993	1	US-08-348-143-1
32	110.5	2.9	993	1	US-08-571-785-1
33	110.5	2.9	993	3	US-09-192-435-1
34	110.5	2.9	993	4	US-09-558-340-1
35	109	2.8	998	2	US-08-449-645A-20
36	109	2.8	998	2	PCT-US95-04681-20
37	109	2.8	998	5	US-08-702-367A-20
38	102	2.7	838	4	US-09-949-016-9916
39	102	2.7	838	4	US-09-949-016-9917
40	101	2.6	990	4	US-09-949-016-10562
41	100	2.6	619	4	US-09-902-540-14749
42	99	2.6	595	1	US-08-468-036-3
43	99	2.6	595	2	US-08-376-843-3
44	99	2.6	970	4	US-09-538-092-664
45	98.5	2.6	564	4	US-09-949-016-6898

ALIGNMENTS

RESULT 1

US-09-747-259-18

; Sequence 18, Application US/09747259

; Patent No. 6569645

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Hanzhong

; APPLICANT: Hillan, Kenneth

; APPLICANT: Tumas, Daniel

; APPLICANT: VanLookeren, Menno

; APPLICANT: Vandlen, Richard

; APPLICANT: Watanabe, Colin

; APPLICANT: Williams, F. Mickey

; APPLICANT: Wood, William

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: 11-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C1P1(US)

; CURRENT APPLICATION NUMBER: US/09/747,259

; CURRENT FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: US 09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/172,096

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: PCT/US99/31274

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: US 60/175,481

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: PCT/US00/04341

; PRIOR FILING DATE: 2000-02-18

; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 60/191,007

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: PCT/US00/07532

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: PCT/US00/15264

; PRIOR FILING DATE: 2000-06-02

; PRIOR APPLICATION NUMBER: US 60/213,087

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: US 09/644,848

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

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, PRIOR APPLICATION NUMBER: US 60/242,837
, PRIOR FILING DATE: 2000-10-24
, PRIOR APPLICATION NUMBER: PCT/US00/30873
, PRIOR FILING DATE: 2000-11-10
, PRIOR APPLICATION NUMBER: US 60/253,646
, PRIOR FILING DATE: 2000-11-28
, PRIOR APPLICATION NUMBER: PCT/US00/32678
, PRIOR FILING DATE: 2000-12-01
, NUMBER OF SEQ ID NOS: 39
, SEQ ID NO 18
, LENGTH: 728
, TYPE: PRT
, ORGANISM: Homo Sapien
US-09-747-259-18

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Query Match	96.7%;	Score 3703;	DB 4;	Length 728;
Best Local Similarity	96.7%;	Pred. No. 0;		
Matches 702: Conservative	2;	Mismatches	8;	Indels 14; Gaps 2;

Qy	7	RMKAAAPRLCVANE - GVGPSASNSGLYNTFKYDNC	TTYLNPVGKVIADAQNITISQY	65
Db	3	RASAGVPALLFVSGEQGVGPSASNSGLYNTFKYDNC	TTYLNPVGKVIADAQNITISQY	62
Qy	66	ACHDQAVTTIWSFGALGIEPLKGFVILEBKSEGRCQQLILKDPKQLNSSPKFGME	125	
Db	63	ACHDQAVTTIWSFGALGIEPLKGFVILEBKSEGRCQQLILKDPKQLNSSPKFGME	122	
Qy	126	SQPFPLNMKFETDYKVVVPFPIKNSNYHFFPFRTRACDLLLPDNLACKPFWKPRNLN	185	
Db	123	SQPFPLNMKFETDYKVVVPFPIKNSNYHFFPFRTRACDLLLPDNLACKPFWKPRNLN	182	

Qy	186	ISQ	-----HGSQMQVSGFDHAPHNFGFRFFYLHKLKHEGPFKKKLCQEQTI	233
Db	183	ISQHSQMQVSGFDHAPHGSDMQVSGFDHAPHNFGFRFFYLHKLKHEGPFKKKLCQEQTT	242	
Qy	233	BTTSCLLQNVSPGDIYIELVDDTTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAF	292	
Db	243	EMTSCLLQNVSPGDIYIELVDDTTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAF	302	
Qy	293	ATLFTVWCRKKQQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNV	352	
Db	303	ATLFTVWCRKKQQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNV	362	
Qy	353	VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIOKIHESQFIIVVCSKGMKYFVDKK	412	
Db	363	VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIOKIHESQFIIVVCSKGMKYFVDKK	422	
Qy	413	NYKHGGGRGSGKGELFLVAVSAIAEKLRAQAKQSSAALSXFLVYFYSCEGDVPGILD	472	
Db	423	NYKHGGGRGSGKGELFLVAVSAIAEKLRAQAKQSSAALSXFLVYFYSCEGDVPGILD	482	
Qy	473	LSTKYRLMDNLPQICSHLHSDHGLQEPGQHTROGSRRENYFRSKSGRSLYVAICNMHQFI	532	
Db	483	LSTKYRLMDNLPQICSHLHSDHGLQEPGQHTROGSRRENYFRSKSGRSLYVAICNMHQFI	542	
Qy	533	DEEPPWFQKQVPFHPPLRYREPVLEKFDGSLVLDVNCXKPGPESDFCLKVEAAVLGAT	592	
Db	543	DEEPPWFQKQVPFHPPLRYREPVLEKFDGSLVLDVNCXKPGPESDFCLKVEAAVLGAT	602	
Qy	593	GPADSQHESQHGGLDQDGEARPALDGSAAQLPLLHTVXAGSPSDMPRDSGIVDSSVPSSSE	652	
Db	603	GPADSQHESQHGGLDQDGEARPALDGSAAQLPLLHTVXAGSPSDMPRDSGIVDSSVPSSSE	662	
Qy	653	LSLFLMEGLSTDQTETSSLTESVSSSGLGEEPPALPSKLLSGSGCKADLCGRSYTDEL	712	
Db	663	LSLFLMEGLSTDQTETSSLTESVSSSGLGEEPPALPSKLLSGSGCKADLCGRSYTDEL	722	
Qy	713	HAVAPL 718		
Db	723	HAVAPL 728		

RESULT 2

US-09-816-744-18
; Sequence 18, Application US/09816744
; Patent No. 6579520
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P2 (US)
; CURRENT APPLICATION NUMBER: US/09/816,744
; CURRENT FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 18
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-816-744-18

Query Match	96.7%;	Score 3703;	DB 4;	Length 728;
Best Local Similarity	96.7%;	Pred. No. 0;		
Matches	702;	Conservative 2;	Mismatches 8;	Indels 14;
Gaps	2;			
QY	7	RMKAAAPRLCAVNE -GVGPASRNSGLYNI	TFKYDNC	TTYLNPVGKHVIADAQNITISQY 65
Db	3	RASAGTVPALFVSGEGVGPASRNSGLYNI	TFKYDNC	TTYLNPVGKHVIADAQNITISQY 62
QY	66	ACHDQAVVITLWSPALGIEFLKGRVILEL	KSEGROCOOLILKDPQLNSSFRTGME 125	
Db	63	ACHDQAVVITLWSPALGIEFLKGRVILEL	KSEGROCOOLILKDPQLNSSFRTGME 122	
QY	126	SQPLNMKFETDYFVKVVPVPSIKNESNYH	FFPTRACD	LLLOPDNLACKPFMKPRNLN 185
Db	123	SQPLNMKFETDYFVKVVPVPSIKNESNYH	FFPTRACD	LLLOPDNLACKPFMKPRNLN 182
QY	186	ISO-----HGSDMQV	SFDHAPHNFGFRFFYLHYLKH	HEGPFKRKTKQEQTT 232
Db	183	ISOHGSDMQV	SFDHAPHNFGFRFFYLHYLKH	HEGPFKRKTKQEQTT 242
QY	233	ETTSCLLQNVSPGDYIIELVDDTNTTRK	QMYHALKPVHSPWAGPIRAVAITVPLVVISAF 292	
Db	243	EMTSCLLQNVSPGDYIIELVDDTNTTRK	QMYHALKPVHSPWAGPIRAVAITVPLVVISAF 302	
QY	293	ATLFTVMCRKKQQENIYSHLDEESSESTY	TAALPRERLPRPKVFLCYSSKDGQGNHNV 352	
Db	303	ATLFTVMCRKKQQENIYSHLDEESSESTY	TAALPRERLPRPKVFLCYSSKDGQGNHNV 362	
QY	353	VQCFAYFLQDFCGCEVALDLMEDFSLC	REGREWVIQIHESQFIIVVCSKGMYFVDKK 412	
Db	363	VQCFAYFLQDFCGCEVALDLMEDFSLC	REGREWVIQIHESQFIIVVCSKGMYFVDKK 422	
QY	413	NYKHGGGSGKGKELFLVAVSAEKLROAK	QSSSAALSXFIAYFYDSCGDVPGILD 472	
Db	423	NYKHGGGSGKGKELFLVAVSAEKLROAK	QSSSAALSXFIAYFYDSCGDVPGILD 482	
QY	473	LSTKYRLMDNLPOLCSHLHSDHGLQEP	QGHTRQGSRRNYFRSKSGRSLYVAICNMHQFI 532	
Db	483	LSTKYRLMDNLPOLCSHLHSDHGLQEP	QGHTRQGSRRNYFRSKSGRSLYVAICNMHQFI 542	
QY	533	DEEPDWFQKQVFPFHPPLRYREPVLEK	PDFSGVLNDVMCRPGPESDFCLKVEAAVLGT 592	

Db 543 DEEDWFEKQVPPHPPPLRYREPVEKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 602
Qy 593 GPADSOHESQGGGLDQGEARPALDGSAAQLOPLHTVKAGSPMDPRDSGIYDSSVPSSE 652
Db 603 GPADSOHESQGGGLDQGEARPALDGSAAQLOPLHTVKAGSPMDPRDSGIYDSSVPSSE 662
Qy 653 LSLPLMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGCGRSYTDEL 712
Db 663 LSLPLMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGCGRSYTDEL 722
Qy 713 HAVAPL 718
Db 723 HAVAPL 728

RESULT 3
US-08-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fangelow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-620-694A-10

Query Match 8.1%; Score 312; DB 2; Length 866;
Best Local Similarity 23.1%; Pred. No. 1,4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
Qy 34 NITFYDNC--TYYLNPVKGKVIADAQNIT-----ISQYACHDQ-----VAVTIWLS 78
Db 49 NCTVKNSTCLDSDWIHP-----RNLTSPSPKDLQQLHFAHTQQGDLFPVAHIEWT 99

Qy 79 -PGALGIEFLKGRFVILBELKSEGRQCOQIILKDPKQOLNSSFKRTGMSQFFPLNMKEETD 137
Db 100 LQTDASILYLEGAELSVLQNTNERLCVR--FBFLSKLRHHRRWRFTFHFV--VDPDQE 156
Qy 138 YFKVY--VPPSPKSNESNYHPFRFRACDILLQPDNLACK---PFWKPRNL----- 184
Db 157 YEYVTHLKPPIPDGPNHOSKNFLVPDCEHARKMKTTPCMSSGSLMDP--NITVETLEAH 215
Qy 185 -----NISQGSMDQVSFDHAPHNFCFRFFYLYHLKHEGPFKRTCKKQRTTETT 235
Db 216 QLRSVFTLWNESHYQILLTSFPMENHSCFEHMH-HI PAPRPEEPHORSNVTLTLNLK 274
Qy 236 SCLLQNVSPGDYIIELVDDT---NTRKVMHYALKVHSPWAGPIRAVAITVPLVVISAF 292
Db 275 GCCRHQVQIQPFSSCLNDCLRHSATVSCPEMDTPEPIPDYMLPYWYFITGISILLVG 334
Qy 293 ATLFTVMCRKKQENIYSHLDESSSSTYTAALPRERLRPR-----KVFLCYSSKDGON 348
Db 335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPADLIPPLKPKRWIIYSA--DHPL 390
Qy 349 HMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREW----IQKHESQFIIVVCSKG 404
Db 391 YVDVLKFAQFLLTACGTEVALDLLEQAISEAGVMTWVGRQEMVESNSKIIIVLCRG 450
Qy 405 MKYFVDKKNYKHKGKGG-----RSGKGELFLVAVSAIAEKURQAKQSSSAALSXPIA 456
Db 451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDLFATAAMNMLPDPKR-----PACFGTYV 501
Qy 457 VYP-DYSCEDGVPGILDSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROG---SRNYF 513
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFBFV--YFRIQDLEMPQPGRMHVRGELSGDNYL 559
Qy 514 RSKSGRSLYVAICNMHOFIDBEPDWF-----KQVFPHPPLRYRBPVLEKFDGSL 565
Db 560 RSPGRLRAALDRFRDWQVRCDFECENLYSADDQDAPSLDEV--FEPELPP-GTGI 617
Qy 566 VLNDVMCKPGPESDFCLKVRAAVLGATGPADSOHE-----SOHGG 605
Db 618 VKRAPLVRE-PGSAQCLAIIDPLVGEEGA-AVAKLEPHLQPRGQAPQPLHTLVLAABEGA 676
Qy 606 LDQDGEARPALDGSAA--ALQ-----PLHTVKAGSPMDPRDSGIYDSSVPSSESLP 656
Db 677 LVAAVEPGPLADGAARLALAGEGEACPLLGSPAG-----RNSVLV---LPVDPEDSP 727
Qy 657 LMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 4
US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fangelow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:  USN 08/620,694
; APPLICATION NUMBER:  USN 08/620,694
; FILING DATE:  21 MARCH 1996
; APPLICATION NUMBER:  USN 08/538,765
; FILING DATE:  7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  USN 08/410,535
; FILING DATE:  23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME:  Perkins, Patricia Anne
; REGISTRATION NUMBER:  34,695
; REFERENCE/DOCKET NUMBER:  2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (206)587-0430
; TELEFAX:  (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-255-10

Query Match      8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

Qy      34 NITPKYDNC--TTVLNPVKGHVIAADQNIT-----ISOYACHDO-----VAVTILWS 78
Db      49 NCTVKNSTCLDDSWHP-----RNLTPSSPKDLQIQLFHAHTQOQDLFPVAHLEWT 99

Qy      79 -PGALGIEFLKGFVRVILEELKSEGRQCOQILKDPKQINSSFKRTGMSQFPLNMKPFETD 137
Db      100 LQTDASILYLEGAELSVLQLTNTERLCVR--FEFLSKLRHHHRWRFTFSHFV-VDPDQE 156

Qy      138 YFVKV--VPFPIKSNESNYHFFRTRACDILLQPDNLACK---PFWKPRNL-----184
Db      157 YEVTVHHLKPIPDGDPNHQSKNPLVPDCEHARMKVITTPCMSSGSLWDP-NITVETLEAH 215

Qy      185 -----NISQSGDMOVFDFAPNFRFRFYLHYKLKHEGPFKRKCKQCKQTETT 235
Db      216 QLRVSFTLNSTHYQILLTSFPWENHSCFEHMH-HIPAPRPEFHQRSNVITLNLK 274

Qy      236 SCLLQNVSPGYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAF 292
Db      275 GCCRHHQVQIQPFSSCLNCLRHSAATVSCPEMPDTPPIPDYMLVWVWFTIGISILLVG 334

Qy      293 ATLFTVMCRKKQENIYSHLDESSSESTYTAALPRELRRP-----KVFLCYSKDQON 348
Db      335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPLPLKPRKVIYISA-DHPL 390

Qy      349 HMNVVQCFAFLQDFCGCEVALDWDWEDFSLCREQEWV---IQKHESQFIIVWCSKG 404
Db      391 YVDVWLKFAQLLFTACGTEVALDLLEEQAISEAGVMTWVGKQKQEMVESNKIILVCSRG 450

Qy      405 MKYFVDKKNYKHKGKG-----RGSGKGELFLVAVSAIAEKLRQAKQSSAALSXFIA 456
Db      451 TR----AKWQALLGRGAPVRLRCDHGPVKGDLFTAAMNMLPDPFR-----PACFGTVV 501

Qy      457 VYF-DYSCGEGDVGILLSTKYRLMDNLPQLCSHLHSDHGLQBPQGHTROG--SRNYP 513
Db      502 CYFSEVSCDGVDPDLFGAAPRYPLMDRPEEV--YFRIQDLEMFQFGRMHRVGLSGDNYL 559

Qy      514 RSKGRSLYVAICNMHOFIDEEPWF-----KQVPPHPPPLRYREPVLEKFPDGL 565
Db      560 RSPGRQLRALDRFRDQVRCDFWECENIYSADDQDAPSLDEV-FEELPLP-GTGI 617

Qy      566 VLNDVMCKPGESDFCLKVEAAVLGATGPADSQHE-----SQHGG 605
Db      618 VKRAPLVRE-FGSQACLAIDPLVGBEGGAIVAKLEPHLQPRGPQAPQPLHTLVLAABEGA 676

;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:  USN 08/620,694
; APPLICATION NUMBER:  USN 08/620,694
; FILING DATE:  21 MARCH 1996
; APPLICATION NUMBER:  USN 08/538,765
; FILING DATE:  7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  USN 08/410,535
; FILING DATE:  23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME:  Perkins, Patricia Anne
; REGISTRATION NUMBER:  34,695
; REFERENCE/DOCKET NUMBER:  2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (206)587-0430
; TELEFAX:  (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-255-10

Query Match      8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

Qy      606 LDQGEARFALDGA---ALQ-----PLLHTYKAGSPSPMDPRDSGIYDSVSPSSLSLP 656
Db      677 LVAAVEGPLADGAAYRLALAGEGEACPLLGSPGAG-----RNSVLFF---LPVDPEDSP 727

Qy      657 IMEGLSTDQTETSSLTESVSSSGLGEBEPPALPSPKLLSGSGCKADLGC 705
Db      728 L--GSSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGGC 768

RESULT 5
US-09-022-696-10
; Sequence 10, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  USN 08/410,535
; FILING DATE:  23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-696-10

Query Match      8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

Qy      34 NITPKYDNC--TTVLNPVKGHVIAADQNIT-----ISOYACHDO-----VAVTILWS 78
Db      49 NCTVKNSTCLDDSWHP-----RNLTPSSPKDLQIQLFHAHTQOQDLFPVAHLEWT 99

Qy      79 -PGALGIEFLKGFVRVILEELKSEGRQCOQILKDPKQINSSFKRTGMSQFPLNMKPFETD 137
Db      100 LQTDASILYLEGAELSVLQLTNTERLCVR--FEFLSKLRHHHRWRFTFSHFV-VDPDQE 156

Qy      138 YFVKV--VPFPIKSNESNYHFFRTRACDILLQPDNLACK---PFWKPRNL-----184
Db      157 YEVTVHHLKPIPDGDPNHQSKNPLVPDCEHARMKVITTPCMSSGSLWDP-NITVETLEAH 215
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185 QY -----NISOHSDMOVSDFHAPHNFGFRFFYLHYKLKHEGPFKRKCKQEQOTTETT 235
Db QLRVSFTLWNESTHYQIILTSFPHMNSCEHMH-HIPAPRPEEFHORSNVTLRLNLK 274
QY SCLLQNVSPGYIIBLVDT---NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
Db GCRHQVQIQPFSSCLNCLRHSAIVSCPEMPDTPPIPYMPLWVWFITGSIILVAG 334
QY ATLFTVMCRKQOENIYSHLDESESSSTYTAALPRERLRPP-----KVFLCYSKQGN 348
Db SVILLIVCMWRLAGPGS---EKYSDDTKYTDGLPAADLIPLPKPRKVIYISA-DHPL 390
QY 349 HNVVQCFAYFLQDFCGCEVALDLWEDFSLCREQREW---IQKHESOFIIVVCSKG 404
Db 391 YDVVVKFAQFLITACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
QY 405 MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLRQAKQSSAALSKEFIA 456
Db 451 TR-----AKQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKR-----PACFGTYV 501
QY 457 VYF-DYSCGDPVPGILDSTKYRLMDNLPLQCSHLHSDHGLQBPQHTROG--SRRNYF 513
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRHVRVGEISGDNYL 559
QY 514 RSKGRSLYVAICNMHQIIDEEDWFE-----KQFVPHPPPLRYREPVLKFDGSL 565
Db 560 RSPGGRQLRAALDRFRDQVRCDFECENYSADDDQAPSLDERV-FEELPLPP-GTGI 617
QY 566 VLNDVMCKPGPSDFCLKVEAAVLGATGPADSQHE-----SQRGG 605
Db 618 VKRAPLVRE-PCSQACLAIPLVGEAGAAVAKLEPHLQPRQAPQPLHTLVLAEEGA 676
QY 606 LDQGEARPALDGA---ALQ-----PLLHTVKGSPDMRDSGIVDSSVPSSELSIP 656
Db 677 LVAAVEPGPLADGAARLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
QY 657 LMEGLSTQDTETSSLTESVSSSGLEGEPEPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMULSFEQSLSCQAQGGC 768

RESULT 6

US-08-978-773-4
; Sequence 4, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Troutt, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/978, 773
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2623-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-773-4

Query Match 8.1%; Score 312; DB 3; Length 866;

Best Local Similarity 23.1%; Pred. No. 1.46-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 34 NITKYDNC--TTLNVPVGHVIADAONIT-----ISOYACHDO-----VAVTILWS 78
Db 49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDIQIQLHFAHTQOQDLPFVAHIEWT 99
QY 79 -PGALGIEFLKGFVRVILEELKSEGRQOQLIKDPKQNSFSKRTGMSQPFLNMKPTD 137
Db 100 LOTDASILYLEGAELSVLQNTNEELCVR--FEFLSKLRHHRRWRFTFSHFV--VDPDQE 156
QY 138 YFVKV--VPPFSIKNESNYHPFPRTRACDLLLLQPDNLAK---PFWKPRML-----184
Db 157 YEVTVHLKPIPDGDPNHQSKNLPDPCHEARMKVITTPCMSSGSLMDP-NITVETLEAH 215
QY 185 -----NISOHSDMOVSDFHAPHNFGFRFFYLHYKLKHEGPFKRKCKQEQOTTETT 235
Db 216 QLRVSFTLWNESTHYQIILTSFPHMNSCEHMH-HIPAPRPEEFHORSNVTLRLNLK 274
QY 236 SCLLQNVSPGYIIBLVDT---NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
Db 275 GCRHQVQIQPFSSCLNCLRHSAIVSCPEMPDTPPIPYMPLWVWFITGSIILVAG 334
QY 293 ATLFTVMCRKQOENIYSHLDESESSSTYTAALPRERLRPP-----KVFLCYSKQGN 348
Db 335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDGLPAADLIPLPKPRKVIYISA-DHPL 390
QY 349 HNVVQCFAYFLQDFCGCEVALDLWEDFSLCREQREW---IQKHESOFIIVVCSKG 404
Db 391 YDVVVKFAQFLITACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
QY 405 MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLRQAKQSSAALSKEFIA 456
Db 451 TR-----AKQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKR-----PACFGTYV 501
QY 457 VYF-DYSCGDPVPGILDSTKYRLMDNLPLQCSHLHSDHGLQBPQHTROG--SRRNYF 513
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRHVRVGEISGDNYL 559
QY 514 RSKGRSLYVAICNMHQIIDEEDWFE-----KQFVPHPPPLRYREPVLKFDGSL 565
Db 560 RSPGGRQLRAALDRFRDQVRCDFECENYSADDDQAPSLDERV-FEELPLPP-GTGI 617
QY 566 VLNDVMCKPGPSDFCLKVEAAVLGATGPADSQHE-----SQRGG 605
Db 618 VKRAPLVRE-PCSQACLAIPLVGEAGAAVAKLEPHLQPRQAPQPLHTLVLAEEGA 676
QY 606 LDQGEARPALDGA---ALQ-----PLLHTVKGSPDMRDSGIVDSSVPSSELSIP 656
Db 677 LVAAVEPGPLADGAARLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
QY 657 LMEGLSTQDTETSSLTESVSSSGLEGEPEPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMULSFEQSLSCQAQGGC 768

RESULT 7

US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305

335	SVILLIVCMWRLAGPGS----	EKYSDDTKYTDGLPAADLI	PPPLKPRKRVIIISA-DHPL	399
349	HMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREW----	IQKIHESQFIIVVCSKG	404	
391	YVDVVLKFAQFLLTAGTGEVALDLLEEQAISEAGVMTWVGRQKQEMWESNGKIIVLCSRG	450		
405	MKFYVDKQYKHGGG-----	RSGKGGELFLVAVSAIAEKLRQAKOSSAALSKEIA	456	
451	TR-----AKWQALLGRGAPVRLRCDHGKPVGDIFTAAMNMILPDKR-----	PACFGTYVW	501	
457	VYF-DYSCGEGVPGILDLSLTKYRLMDNLPOLCSHLHSRDHGLQEBQGHTRQG--	SRRYNF	513	
502	CYFSEVSCGDVPDLFGAARPLYLMDRFEV--	YFRIQDLEMFQGRMHRVGEISGDNYL	559	
514	RKSGRSLYVAICNMHQFTIDEPDWFE-----	KQVVPHPPLRYRREPVLKFDSSL	565	
560	RSPGGQLRAALDRFRDQVRCDFECENLYSADDQDAPSLDEEV-FEELPLPP-GTGI	617		
566	VLDVNMCKPGPSDFCLKVAAAVLGATGAPDSQHE-----	SQHGG	605	
618	VKRAPLVRE-PGSOACLAIDPLVGEEGAAVAKLEPHLQPRQPAPQPLHLTLVLAEEGA	676		
606	LDQDGEARPALDGA-----ALQ-----	PLLHTVTKAGSPDMRDSGIYDSSVPSSLSLP	656	
677	LVAAVEPGPLADGAARVRLALAGEACPLLGSPGAG-----	RNSVLF---	LPVDPDESP	727
657	LMEGLSTDQETSTLSTESVSSSGIGEBEPALPKLLSSGSKADLGC	705		
728	L-GSSTPNASPDLLPEDVR-----	EHLEGLMLSLFEQSLSCQAQGC	768	
RESULT 8				
US-09-022-260-10				
; Sequence 10, Application US/09022260				
; Patent No. 6100235				
; GENERAL INFORMATION:				
; APPLICANT: Yao, Zhengbin				
; APPLICANT: Spriggs, Melanie				
; APPLICANT: Fanslow, William				
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17				
; NUMBER OF SEQUENCES: 10				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: Immunex Corporation				
; STREET: 51 University Street				
; CITY: Seattle				
; STATE: WA				
; COUNTRY: USA				
; ZIP: 98101				
; COMPUTER READABLE FORM:				
; MEDIUM TYPE: Floppy disk				
; COMPUTER: Apple Power Macintosh				
; OPERATING SYSTEM: Apple Operating System 7.5.5				
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/09/022,260				
; FILING DATE:				
; CLASSIFICATION:				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: 08/620,694				
; FILING DATE:				
; CLASSIFICATION:				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: USSN 08/410,535				
; FILING DATE: 23 MARCH 1995				
; CLASSIFICATION:				
; ATTORNEY/AGENT INFORMATION:				
; NAME: Perkins, Patricia Anne				
; REGISTRATION NUMBER: 34,695				
; REFERENCE/DOCKET NUMBER: 2617-B				
; TELECOMMUNICATION INFORMATION:				
; TELEPHONE: (206)587-0430				
; TELEFAX: (206)				
; INFORMATION FOR SEQ ID NO: 10:				
; SEQUENCE CHARACTERISTICS:				
; LENGTH: 866 amino acids				
; TYPE: amino acid				
; TOPOLOGY: linear				
; MOLECULE TYPE: protein				
US-09-022-253-10				
Query Match 8.1%; Score 312; DB 3; Length 866;				
Best Local Similarity 23.1%; Pred. No. 1.4e-23;				
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;				
QY	34	NITFKYDNC--TYYLNPVCKHVIADAQNT-----	ISQYACHDQ-----	VAVTILWS 78
DB	49	NCTVKNSTCLDSDTHP-----	RNLTPSSPKDLQILHFAHTQOGDLFPVAHIEWT 99	
QY	79	PGALGIEFLKFRVITBELKSEGRQCOQLILKDPKQLNSSFKRTGMESQPFPLANKFETD 137		
DB	100	LQTDASILYEGAEISVLQNTNELCVR--	FEFLSKURHHRRWRFTFSHFV-VDPDQE 156	
QY	138	YFYKV--VPFPISKNESYHPPFFRTRACDLLLLQPDNLACK---	PFWKPRNL-----	184
DB	157	YEVTVHHLPKPIPDGPNHQSKNFLVPDCEHARMKVITPCWSSGSLWDP-NITVETLEAH 215		
QY	185	-----NISOHSDMQVSPDHAPHNPGFRFFVLYHLYKHGEPFKRKTCKQQTTEYT 235		
DB	216	QLRVSPFTLNWSTHYQILLTSPFMHNSCFEHMH-HIPAPRPEFHQRSNVTLTLRLNK 274		
QY	236	SCLLQNVSPGDIYIELVDDT---	NTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAF 292	
DB	275	GCCRHQVQIQPFSSCLNDCLRHSATVSCPENPDTPPIPIYMPLWVYVFTIGSILVVG 334		
QY	293	ATLFTVCRKKQEQNIYSHLDBESSESSTYTAALPRERLRPRP----	KVFLCYCSKDGQN 348	

SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-10

Query Match 8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 34 NITKYDNC--TTLNVPVGHVIAADQNIT-----ISQYACHDQ-----VAVTILWS 78
DB 49 NCTVKNSTCLDSDSWHP-----RNLTPSSPKDLQILHFAHTQQGLFPVAHIEWT 99

QY 79 -PGALGIEFLKGFVILBEELKSEGRQCOQLILKPKQLNSSFKRTGMSQPLNKKFTD 137
DB 100 LQTDASILYLEGAEELSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDOE 156

QY 138 YFVKV--VPPPSIKNESNYHPPFRFTRACDLLLLQPDNLACK---PFWKPRNL----- 184
DB 157 YEVTVHLLPKIPDGDPNHQSKNFLVPDCEHARMKVTPPCMSGSLMDP-NITVETLEAH 215

QY 185 -----NISQHGSDMVQSFDAHFNFGFRFFYLHYKLHKGFFKRTCKQEQTTETT 235
DB 216 QLRVSFTLWNESTHYQILLTSFPHMNHSCFEHMH-HIPAPRPEFHQSRNVTLTLRNLK 274

QY 236 SCLLQNVSPGYIILVDDT---NTRTKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 275 GCCRHOVQIQPFSSCLNCLRHSAVSCPEMPDTPPIPYMPLVWYVFTGISLLVG 334

QY 293 ATLFTVMCRKKQENIYSHLDESESESTYTAALPRELRPRP-----KVFLCYSKSQGN 348
DB 335 SVILLIVCMWRLAGPGS---EKSDDTKYTDGLPAADLIPLPKPRKWIYISA-DHPL 390

QY 349 HNVVQCFAFLQDFCGCEVALDLWEDFSLCREGREW----IQKHESQFIIVVCSKG 404
DB 391 YDVLVLFKAQFLLTACGTVEALDLLEEQAISEAGVWTVGKQKQEMVESNKIIVLCSRG 450

QY 405 MKYFVDKKNYKHGGG-----RSGKGBELFLVAVSAIAEKLRQAKQSSAALSKEFIA 456
DB 451 TR-----AKWQALLGRGAPVRLRCDHGKPGVGLDFTAAAMNMLPDKR-----PACFGTYV 501

QY 457 VYF-DYSCGEGVPGILDSTKYRLMDNLPOLCSHLHSDHGLQBPQOHTROG--SRRNYF 513
DB 502 CYFSEVSCDGVDPDLFGAAPTPLMDRFEV--YFRIQDLEMFQGRHVRGELSGDNYL 559

QY 514 RSKGRSLYVAICNNHQFIDEEPWF-----KQFVFPHPPLRYREPVEKFDGL 565
DB 560 RSPGGRQLRALDRFDQVRCDFWECENLYSADDQDAPSLDEEV-FEELPLPP-GTGI 617

QY 566 VLNDVMCKGPBSPCLKVEAAVLGATPADSQHE-----SQHGG 605
DB 618 VKRAPLVRE-PGSQACLAIPLVGBEGGAATAKLEPHLQPRGPAPQPLHTLVLAABEGA 676

QY 606 LDQGEARALDGS---ALQ-----PLHTVKAGSPDMRDSIGIYDSSVESSELSLP 656
DB 677 LVAAVEPGLADGAARVALAGEACPLLGSPGAG-----RNSVLP---LPVDPDPS 727

QY 657 LMEGLSTQDTSTSLTESVSSSGLGEPEPPALPSKLLSSGCKADLGC 705
DB 728 L--GSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGGC 768

RESULT 9

US-09-022-259-10
Sequence 10, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-259-10

Query Match 8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 34 NITKYDNC--TTLNVPVGHVIAADQNIT-----ISQYACHDQ-----VAVTILWS 78
DB 49 NCTVKNSTCLDSDSWHP-----RNLTPSSPKDLQILHFAHTQQGLFPVAHIEWT 99

QY 79 -PGALGIEFLKGFVILBEELKSEGRQCOQLILKPKQLNSSFKRTGMSQPLNKKFTD 137
DB 100 LQTDASILYLEGAEELSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDOE 156

QY 138 YFVKV--VPPPSIKNESNYHPPFRFTRACDLLLLQPDNLACK---PFWKPRNL----- 184
DB 157 YEVTVHLLPKIPDGDPNHQSKNFLVPDCEHARMKVTPPCMSGSLMDP-NITVETLEAH 215

QY 185 -----NISQHGSDMVQSFDAHFNFGFRFFYLHYKLHKGFFKRTCKQEQTTETT 235
DB 216 QLRVSFTLWNESTHYQILLTSFPHMNHSCFEHMH-HIPAPRPEFHQSRNVTLTLRNLK 274

QY 236 SCLLQNVSPGYIILVDDT---NTRTKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 275 GCCRHOVQIQPFSSCLNCLRHSAVSCPEMPDTPPIPYMPLVWYVFTGISLLVG 334

QY 293 ATLFTVMCRKKQENIYSHLDESESESTYTAALPRELRPRP-----KVFLCYSKSQGN 348
DB 335 SVILLIVCMWRLAGPGS---EKSDDTKYTDGLPAADLIPLPKPRKWIYISA-DHPL 390

QY 349 HNVVQCFAFLQDFCGCEVALDLWEDFSLCREGREW----IQKHESQFIIVVCSKG 404
DB 391 YDVLVLFKAQFLLTACGTVEALDLLEEQAISEAGVWTVGKQKQEMVESNKIIVLCSRG 450

QY 405 MKYFVDKKNYKHGGG-----RSGKGBELFLVAVSAIAEKLRQAKQSSAALSKEFIA 456

Db 451 TR-----AKWQALLGKGAFLVRLCDHGKPVGDLFTAAWMLLPDPKX-----PACFGYVW 501
Qy 457 VYF-DYSCGDPVGLDSTKYRLMDNLPQLCSHLHSDHGLQBPQHTROG--SRNYF 513
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRPEEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 514 RSKGRSLYVAICNMHQFIDEEPWFE-----KQVPHPPPLRYREPVLKFDGSL 565
Db 560 RSPGGRQJRAALDRFRDQVRCDFWECENLYSADDQDAPSLDEEV-FEPLLP-GTGI 617
Qy 566 VLNDVMCKPGSPDCLKVEAAVLGATGPADSOHE-----SQHGG 605
Db 618 VKRAPLVRE-PGSOACLAIDPLVGEAGAAVAKLEPHLQPRGQAPQPLTLVLAABEGA 676
Qy 606 LDQDGEARPALDGS-----ALQ-----PLLHTVKAGSPDMPRDSGIYDSSVPSSELSLP 656
Db 677 LVAAVEPGPLADGAARVRLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
Qy 657 LMEGLSTDQTTSTSLTESVSSSGLGEEPPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 10

US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-257-10

Query Match 8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
Qy 34 NTFKYDNC--TTLNPNVGVKHVIADAQNIT-----ISOYACHDQ-----VAVTILWS 78
Db 49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDLQIQLHFAHTQQGDLFFVAHIEWT 99
Qy 79 -PGALGTEFLKGRVRIIEELKSEGRQCOQLILDKPOLNSSFYKRTGMSQPELNMKMETD 137
Db 100 LQTDASLYLEGAELSVLQNTNERLCVR--FBFLSKLRHHRRWRFTFHFV-VDPDQE 156
Qy 138 YFVKV--VPPFSIKNESNYHPFFRTRACDLQLLQPDNLACK---PFWKPRNL----- 184
Db 157 YEVTVHLHPKIPDGDPNHQSKNPLVPDCEHARKVTTTPCMSSGSLWDP-NITVETLEAH 215
Qy 185 -----NISQHSMDQVSDFHAPHNFRFRFYLYHKLKHEGPPKCKTKQBOQTETT 235
Db 216 QLRVSTPLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRDEEFPQRSNVTLTLRLNK 274
Qy 236 SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
Db 275 GCCRHQVQIQIPFFSSCLNCLRHSAVSCEMPDTPPEIPDYWPLWYVWITGISILVG 334
Qy 293 ATLFTVMCRKKQOBENIYSHLDESSSESTYTAALPRERLRPRP-----KVFLCYSSKDGQN 348
Db 335 SVILLIVCMTRWLAGPGS---EKYSDTKYTDGLPAADLPPPLKPKRWIIISA-DHPL 390
Qy 349 HMNVOCFAYFLQDFCGCEVALDLMEDFSLCREGQREW---IQKIHESQFIIVVCSKG 404
Db 391 YVDVVLKFAQFLLTACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
Qy 405 MKYFVDKKNYKHGGG-----RSGKGELFLVAISAIAEKLRQAKQSSAALSXFIA 456
Db 451 TR-----AKWQALLGKGAFLVRLCDHGKPVGDLFTAAWMLLPDPKX-----PACFGYVW 501
Qy 457 VYF-DYSCGDPVGLDSTKYRLMDNLPQLCSHLHSDHGLQBPQHTROG--SRNYF 513
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRPEEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 514 RSKGRSLYVAICNMHQFIDEEPWFE-----KQVPHPPPLRYREPVLKFDGSL 565
Db 560 RSPGGRQJRAALDRFRDQVRCDFWECENLYSADDQDAPSLDEEV-FEPLLP-GTGI 617
Qy 566 VLNDVMCKPGSPDCLKVEAAVLGATGPADSOHE-----SQHGG 605
Db 618 VKRAPLVRE-PGSOACLAIDPLVGEAGAAVAKLEPHLQPRGQAPQPLTLVLAABEGA 676
Qy 606 LDQDGEARPALDGS-----ALQ-----PLLHTVKAGSPDMPRDSGIYDSSVPSSELSLP 656
Db 677 LVAAVEPGPLADGAARVRLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
Qy 657 LMEGLSTDQTTSTSLTESVSSSGLGEEPPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 11

US-09-549-679-10
; Sequence 10, Application US/09549679
; Patent No. 6680057
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,679
FILING DATE: 14-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-549-679-10

Query Match 8.1%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
QY 34 NITPKYDNC--TYYLNPVGVKHVIADAQNT-----ISOYACHDQ-----VAVTIILWS 78
DB 49 NCTVKNSTCLDDSWIHP-----RNLTSSPKDLQIQLHFAHTQGDLPFVAHIEWT 99
QY 79 -PGALGIEFLKGFVILSELKSEGRQCQQLILKDPKQNSSFKRTGMSQPLNKKFTD 137
DB 100 LQTDASILYLEGAELSVLQANTNERLCVR--FEFLSKLRHHRRWRFTFSHFV--VDPDOE 156
QY 138 YFVKV--VPFPIKSNESYHPPFTRACDILLQDNLACK---PFWKPRNL-----184
DB 157 YEVTVHLLPKPIPDGDPNHQSKNFLVPDCEHARMKVITTPCMSGSLWDP-NITVETLEAH 215
QY 185 -----NISQSGDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 235
DB 216 QLRSVFTLWNESTHYQILLTSPPHENHSCFEHMH-HIPAPRPEEFHORSNVTLRLNLK 274
QY 236 SCLLQNVSPGDYIIELVDDT---NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 275 GCCRHOVQIQPFSSCLNCLRHSAVSCPEMPDTPPEIPDYMWPLWYVFWFITGISILLVG 334
QY 349 HNNVQCFAYFLQDFCGCEVALDLWEDFSLCREGQEWV----IQIHESQFIIVVCSKG 404
DB 391 YVDVVLKFAQLLTACGTEVALDLLEEQAISEAGVMTWGRQKQEMVESNSKIIIVLCRSG 450
QY 405 MKYFVDKKNYKHKGKGG-----RSGSGELFLVAVSAIAEKLRQAQKSSAALSFKTIA 456
DB 451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMLPDFKR-----PACFGTYV 501
QY 457 VYF-DYSCGDVPGILDSTKYRLMDNLPQLCSHLHSDHGLQEPGQHTROG--SRRNVF 513
DB 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMPQGRMHRVGEISGDNYL 559
QY 514 RSKSGRLVAICNMHQFIDEFPDWE-----KQFVFPFPPPLRYREPVLKRFDSGL 565

DB 560 RSPGGRQLRAALDRFRDWQVRCPDWFECCENLYSADDQDAPSLDEEV-FEELPLPP-GTGI 617
QY 566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE-----SQHGG 605
DB 618 VKRAPLVRE-PSQACLAIDPLVCEEGGAAVAKLEPHLQPRGQPAQPLHTLVLAABEGA 676
QY 606 LDQGEARPALDGA---ALQ-----PLLHTVAGSPDMPSRSGIYDVSVPSELSLP 656
DB 677 LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPAG-----RNSVLFP--LPVDPEDSP 727
QY 657 LMEGLSLDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSCCKALGC 705
DB 728 L--GSSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGGC 768
RESULT 12
US-10-033-522-1
; Sequence 1, Application US/10033522
; Patent No. 6793919
; GENERAL INFORMATION:
; APPLICANT: MOHLER, Kendall M.
; TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists
; FILE REFERENCE: 2982-A
; CURRENT APPLICATION NUMBER: US/10/033,522
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: US 60/241,230
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-522-1

Query Match 8.1%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
QY 34 NITPKYDNC--TYYLNPVGVKHVIADAQNT-----ISOYACHDQ-----VAVTIILWS 78
DB 49 NCTVKNSTCLDDSWIHP-----RNLTSSPKDLQIQLHFAHTQGDLPFVAHIEWT 99
QY 79 -PGALGIEFLKGFVILSELKSEGRQCQQLILKDPKQNSSFKRTGMSQPLNKKFTD 137
DB 100 LQTDASILYLEGAELSVLQANTNERLCVR--FEFLSKLRHHRRWRFTFSHFV--VDPDOE 156
QY 138 YFVKV--VPFPIKSNESYHPPFTRACDILLQDNLACK---PFWKPRNL-----184
DB 157 YEVTVHLLPKPIPDGDPNHQSKNFLVPDCEHARMKVITTPCMSGSLWDP-NITVETLEAH 215
QY 185 -----NISQSGDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 235
DB 216 QLRSVFTLWNESTHYQILLTSPPHENHSCFEHMH-HIPAPRPEEFHORSNVTLRLNLK 274
QY 236 SCLLQNVSPGDYIIELVDDT---NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 275 GCCRHOVQIQPFSSCLNCLRHSAVSCPEMPDTPPEIPDYMWPLWYVFWFITGISILLVG 334
QY 293 ATLFTVMCRKQKQENIYSHLDESESSSTYTAALPRELRPRP-----KVFLCYSSKDGON 348
DB 335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVIYISA-DHPL 390
QY 349 HNNVQCFAYFLQDFCGCEVALDLWEDFSLCREGQEWV----IQIHESQFIIVVCSKG 404
DB 391 YVDVVLKFAQLLTACGTEVALDLLEEQAISEAGVMTWGRQKQEMVESNSKIIIVLCRSG 450
QY 405 MKYFVDKKNYKHKGKGG-----RSGSGELFLVAVSAIAEKLRQAQKSSAALSFKTIA 456
DB 451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMLPDFKR-----PACFGTYV 501
QY 457 VYF-DYSCGDVPGILDSTKYRLMDNLPQLCSHLHSDHGLQEPGQHTROG--SRRNVF 513

Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGEISGDNYL 559
Qy 514 RSKGRSLYVAICNMHQFIDREDFE-----KQFVPHPPPLRYREPVLEKFSGL 565
Db 560 RSPGGRQLRAALDRFQWQRCDFWFCENIYSADDDQDAPSLDEB-VFEEPLPP-GTGI 617
Qy 566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHE-----SQHGG 605
Db 618 VKRAPLVRE-PSQACLAIDPLVGEEGA-AVAKLEPHLQPRQAPQPLHTLVLAEEGA 676
Qy 606 LDQGEARPALDGS---ALO-----PLLHTVXAGSPDMRDSGGIYDSSVPSSELSLP 656
Db 677 LVAAVEPGPLADGAARLALAGEGEACFLLGSPGAG-----RNSVLF---LPVDPEDSP 727
Qy 657 LMEGLSTDQTTSSLTSSVSSSGSGLEGEPPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSQAQGGC 768

RESULT 13

US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-620-694A-2

Query Match 8.0%; Score 306; DB 2; Length 864;
Best Local Similarity 22.5%; Pred. No. 6.1e-23;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;
Qy 5 GWRM-----KAAARPRL-----CVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGK 51

Db 17 GWLLLLLNLVLAAPGRASPLLDFFAPVCAQEGSLCRVKNSTCLDDSMWHPKNTLPSSPKNI 76
Qy 52 HVTADAGNITISQYACHQVAVT-ILWS-PGALGIBELKGFVILELKGSEGCQOQ--- 106
Db 77 YI-----NLSVSTQHGELVPVLHVETLTQDASILYLEGAELSVLQNTNERLCVRFQF 131
Qy 107 --LILKDPKOLNSFKRTGMESQPFILNMKFETDYFVKVVPFPSPKINENYHPFFRTRAC 164
Db 132 L\$MLQHRKKWRFSF-----SHFVDPGQGEYEVTVHHLPKPIPDGPNHKSIIIFVDC 185
Qy 165 D---L\$LLQPNLACKPFWKPRNLNI-----SQH-----GSDMOV 195
Db 186 EDSOMKMTTSCVSSGLWDP-NITVETLDTQHLRVDFTLWNESPTYQVLLSEFSDSNHS 244
Qy 196 SFD-----HAPHNFGFRFFYLYKLEKHE---GPFKRKTKCQQTITETCLL 239
Db 245 CFDVVKQIFAPROEEFHQRANVTFTLSKFMCCHHVQVQPF-FSSCLND-----CLR 296
Qy 240 QNVSPGDYIILVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVAITVPLVWISAFATL 295
Db 297 HAVTVPCPVI-----SNVT-----VFKPVADYIPLWYGLITLIAL-----LLVGSVIVL 341
Qy 296 FTVMCRKKQENIYSHLDEESSESTYTAALPRERLPRPKVFLCYSSKQGNHNVQC 355
Db 342 IICMTWRLSGADQEKHGDDSKINGILPVAULTPPPLRPR-KWIVVISA-DHPLYVEVVLK 399
Qy 356 PAYFLQDFCCCEVALDWEDFSICREQOREWVQK-----IHESQFIIVVCSKGMKYFVDK 411
Db 400 FAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQEMVESNSKIIILCSR-----TQ 454
Qy 412 KNYKHGG-----GRGSGKGLFVAVSAIAEKROAKQSSAALSKFIAVIFYDY 461
Db 455 AKWKAILGWABPAVOLRCDHWKPAAGDLFTAAMNMLPDFKR-----PACFGTYVVCYFSG 509
Qy 462 SC-EGDVPGLDLSKYRLMDNLPQLCSHLHSRDHGLQEPQ--HTROGSRNRYFRSKG 518
Db 510 ICSERDVPLFNITSRYPLMDRFEV--YFRIQDLEMFQGRMHRVRELATGDNLYQSPSG 567
Qy 519 RSLYVAICNMHQFIDREDFEKFQFVFHP-----PPLR---YREPVLEKDSGLVNDVM 571
Db 568 ROLKEAVLRFQEWQTCQPDWFERENCLADGQDLPSLDEEVFEDPLLP-GGGIVKQOQL 626
Qy 572 CKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQD-----GEAR 613
Db 627 VREL-P-SDGCLVVDVCV-----SEESRMAKLDPQLMFPQRELVAHTLQSMVLPAEQV 677
Qy 614 PALDGSAAALQPLLHTVXAGSPDMP--RDS-----GIYDSSV---PSSLSLPL----- 657
Db 678 PA---AHVVEPLHLPDGSGAAALPMTEDSEACPLLGVQRNSILCLPVDSDDLPLCSTPM 734
Qy 658 -----MEGLSTDQTTSSLTSSVSSSGLEGEPPP-----ALPSKLLSSGCKADL 704
Db 735 MSPDHQGDAREQLESLMLSVLQOQSLGSPLESFPRPEVLEGTCTPSEEBQORQVQSDQG 794

RESULT 14

US-09-022-255-2
; Sequence 2, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-2

Query Match 8.0%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 6.1e-23;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;

QY 5 GWRM-----KAAARPL-----CVANEGVGPASRNSGLNITFKYDNCCTYLNVPVK 51
Db 17 GWLILLNLVAPGRAPRLDPFAPVCAQEGSCVKNSTCLDDSWIHPKNITPSPKNI 76
QY 52 HVIADAQNITISQYACHDQAVT-ILMS-PGALGIEFLKGFVLEELKSEGRQCOQ--- 106
Db 77 YI-----NLSVSSTQHGLVPLVHVEWTQDASILYLEGABLSVLQNTNERLCVKQF 131
QY 107 --LILKDPQLNSSFRTGMSQPLNMKFEDYFKVVPSPISKESNYHPFFRTAC 164
Db 132 LSQLQHRKRWRFSF-----SHFVDPQEQEYEVTVHHLPKPIPDGDPNHSKIIFVDC 185
QY 165 D---LLQPDNLACKPFWKPRNLNI-----SQH-----GSDMQV 195
Db 186 EDSKRWMTTSCVSSGSLWDP-NITVETLDTQHLRVDFTLWNESTPYQVLLSPSSEVHS 244
QY 196 SPD-----HAPHNFGFRFFYLHYKLKHE--GPPKRTCKQEQTTTTSCLL 239
Db 245 CFDVVKQIFAPQEEFHQRANVTFTLSKPHWCCHHHVQVQPF-FSSCLND-----CLR 296
QY 240 QNVSPGDYIIELVDTNTRKVMHVALXPV--HSP-WA-GPIRAVAITVPLVVISAFATL 295
Db 297 HAVTVPCPVI-----SNIT-----VPKPVADYIPLWVYGLITLAI-----LLVGSVIL 341
QY 296 FIVMCKRQKQENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQNHNVQC 355
Db 342 IICMTWRLSGAOEHGDDSKINGILPVADLTPPLRPR-KWIVIVISA-DHPLYVEVILK 399
QY 356 FAYFLQDFCGCVALDLMEDFSLCRQEWYIQK-----IHBSQFIIVVCSKGMKYFVDK 411
Db 400 FAQFLITACGTEVALDLLEEQVISEVGMVTVSRQKQEWVESNKIILCSRQ-----TQ 454
QY 412 KNYKHKG-----GRSGKGELFLVAVSAIAEKLQAKQSSSALSFIAYVDY 461
Db 455 AKWKAILGWAEPVQLRCDHMKPAGDLFTAAAMNMLPDFKR-----PACFGTYVVCYFG 509
QY 462 SC-EGDVPGILLSTKYRLMDNLPLQCSHLHSDHGLQEPGQ--HTRQSRNRYFRSKSG 518

Db 510 ICSEKRVDFLNFNITSRYFLMDRFEV--YFRIQDLEMFEPGRMHVRELATGDNLYQSPSG 567
QY 519 RSLVVAICNMQHOFIDEEBPDWFEKQFVPFHP---PPLR---YRBPVLEKFPDGLVNDVM 571
Db 568 RQLKEAVLRFOEWOTQCPDWFERNCLADQDLPSLDEEVFEDPLLP-GGGIVKQOPL 626
QY 572 CKPGESDFCLKVEAAVLGATGPADSQHESQHGLDQD-----GEAR 613
Db 627 VRELPSDGLVVDVCV-----SEESRMAKLDPOLWPQRELVAHTLQSMVLPABQV 677
QY 614 PALDGSAAQLPLLHTVKGSPSDMP--RDS-----GIYDSSV---PSSELSLPL----- 657
Db 678 PA---AHVVEPLHLPDGSGAAQLPMTEDSACPLLGVRNSILCLFVDSDDLPLCSTPM 734
QY 658 ----M3GLSTDQETSTSLTESVSSSGCLGEEPP-----ALPSKLLSGSGCKADLG 704
Db 735 MSPDHLDQDAREQLESLMLSVLQSLSQPLESWPRFEVLEGGCTPSEERQSVQSDQG 794

RESULT 15
US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022.696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-696-2

Query Match 8.0%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 6.1e-23;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2005, 00:46:03 ; Search time 2843.82 Seconds
(without alignments)
5436.778 Million cell updates/sec

Title: US-10-717-282-1

Perfect score: 2383

Sequence: 1 ccgcggcgccaccgccac.....aagcattgccacttagctg 2383

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 3244068913 residues

Total number of hits satisfying chosen parameters: 14611516

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2289	96.1	2341	9	US-09-912-157-7
6	2289	96.1	2341	18	US-10-717-282-7
7	2282.6	95.8	4477	20	US-10-842-006-1

8	2282.6	95.8	4477	20	US-10-608-449-1	Sequence 1, Appli
9	2218.6	93.1	2786	10	US-09-863-818A-9	Sequence 9, Appli
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ALIGNMENTS

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; Sequence 1, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2344)
US-09-912-157-1

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; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
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RESULT 5

US-09-912-157-7

; Sequence 7, Application US/09912157

; Patent No. US20020165348A1


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Qy 1981 CCAGCACGAGAGTCAGCATGCGGGCCTGGACCAAGACGGGAGGCCCGGCTCGGACAT 2040
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Db 2299 TTTGTAAACAAACGAAAGAGTCTAAGCATTTAGCTG 2341
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RESULT 6

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US-10-717-282-7
; Sequence 7, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Fresnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2302)
US-10-717-282-7
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Query Match 96.1%; Score 2289; DB 18; Length 2341;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2341; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

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RESULT 7
US-10-842-006-1
; Sequence 1, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
; FILE REFERENCE: MP103-071P1RM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)...(2309)
US-10-842-006-1

Query Match 95.8%; Score 2282.6; DB 20; Length 4477;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2337; Conservative 0; Mismatches 4; Indels 42; Gaps 1;

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Db 2183 CTCTTCAAGGCTGGGTGAGGAGGAACCTCTGCGCTTCTTCCAGCTCTCTCTCTGG 2242
Qy 2281 GTCATGCAAAAGCAGATCTTGGTTCCCGCAGCTACACTGATGAACTCCACGCGGTGCGCCC 2340
Db 2243 GTCATGCAAAAGCAGATCTTGGTTCCCGCAGCTACACTGATGAACTCCACGCGGTGCGCCC 2302
Qy 2341 TTTGTAAACAAACGAAAGAGTCTAAGCATTCGCCACTTTAGCTG 2383
Db 2303 TTTGTAAACAAACGAAAGAGTCTAAGCATTCGCCACTTTAGCTG 2345
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RESULT 8

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US-10-608-449-1
; Sequence 1, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Tsinghua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: I2003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-608-449-1
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Query Match          95.8%; Score 2282.6; DB 20; Length 4477;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2337; Conservative 0; Mismatches 4; Indels 42; Gaps 1;
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Db 2123 GATGGAAGACTCTCGACGGACACAGAGAAACGCTTCCCTGACGGAGACGGTGTCTC 2182
Qy 2221 CTCTTCAGGCCCTGGGTGAGAGAGAACCTTCCTGCGCCCTTCCTTCCAAAGCTCCTCTCTTCTGG 2280
Db 2183 CTCTTCAGGCCCTGGGTGAGAGAGAACCTTCCTGCGCCCTTCCTTCCAAAGCTCCTCTCTTCTGG 2242
Qy 2281 GTCATGCAAAACGAGATCTTGGTGTCCGCGAGCTACACTGATCAATCCACGCGGTGCGCCC 2340
Db 2243 GTCATGCAAAACGAGATCTTGGTGTCCGCGAGCTACACTGATCAATCCACGCGGTGCGCCC 2302
Qy 2341 TTGTGTAACAAACGAAAGAGCTTAAGCAATGCCACTTTAGCTG 2383
Db 2303 TTGTGTAACAAACGAAAGAGCTTAAGCAATGCCACTTTAGCTG 2345

RESULT 9

US-09-863-818A-9
; Sequence 9, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)..(2283)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (118)..()
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (170)..(170)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
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; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
; US-09-863-818A-9

Query Match 93.1%; Score 2218.6; DB 10; Length 2786;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2292; Conservative 0; Mismatches 20; Indels 45; Gaps 2;

Qy 27 CTGGCCAGCGGGCGCGCGGGGCGAGAGAACGGCTTGGCTGGGCGAGCGCACGGCCA 86
Db 11 CGGGCCAGCAGCGGGCGCGCGGGGCGAGAGAACGGCTTGGCTGGGCGAGCGCACGGCCA 70
Qy 87 TGGCCCCGTGGTGCAGCTCTGCTCCGCTCTCTTTTACGGTCAAACGCTGCCTCAACGGCT 146

Db 71 TGGCCCCGTGGTGCAGCTCTGCTCCGCTCTTCTTACGGTCAACGCTGCCTCAACGGCT 130
Qy 147 CGCAGCTGGCTGTGGCCGCTGGCGGGTCCGGCCGCGCGGGGCGCGACACCTTGGCT 206
Db 131 CGCAGCTGGCTGTGGCCGCTGGCGGGTCCGGCCGCGCGGGGCGCGACACCTTGTAGCT 190
Qy 207 GGAGGATGAAAGCGGCTGCCGACCCCGGCTTTGTGTGCTTAATGAGGAGTGGGGCCAG 266
Db 191 GGA-----NGGGAGTGGGGCCAG 208
Qy 267 CCAGCAGAAACAGTGGGCTGTACAAATCACCTTTCAAATATGACAAATGTGTACCACTACT 326
Db 209 CCAGCAGAAACAGTGGGCTGTACAAATCACCTTTCAAATATGACAAATGTGTACCACTACT 268
Qy 327 TGAATCCAGTGGGGAAGCATGTGCTGACGCCCAAGATATCACCATCAGCCAGTATG 386
Db 269 TGAATCCAGTGGGGAAGCATGTGCTGACGCCCAAGATATCACCATCAGCCAGTATG 328
Qy 387 CTTGCCATGACCAAGTGGCAGTCAACATCTTTGCTCCCAAGGGGCGCTCGGCATCGAAT 446
Db 329 CTTGCCATGACCAAGTGGCAGTCAACATCTTTGCTCCCAAGGGGCGCTCGGCATCGAAT 388
Qy 447 TCCTGAAAGGATTTTCGGGTAACTACTGGAGGAGCTGAAAGTCGGAGGGAGACAGTGCCTAAC 506
Db 389 TCCTGAAAGGATTTTCGGGTAACTACTGGAGGAGCTGAAAGTCGGAGGGAGACAGTGCCTAAC 448
Qy 507 AACTGATTTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAAT 566
Db 449 AACTGATTTAAAGGATCCGAAGCAGTCAACAGTAGCTTCAAAAGAACTGGAATGGAAT 508
Qy 567 CTCAACCTTTCTGAAATATGAAATTTGAAACGGATTAATTCGTAAAGGTTCTCCCTTTTC 626
Db 509 CTCAACCTTTCTGAAATATGAAATTTGAAACGGATTAATTCGTAAAG---TTGTCTCTTT 565
Qy 627 CTTCCATTAAACGAAAGCAATTTACCACTCTTTCTTTTAAACCGGAGCTGTGACC 686
Db 566 CTTTCATTAAACGAAAGCAATTTACCACTCTTTCTTTTAAACCGGAGCTGTGACC 625
Qy 687 TGTGTTACAGCCGGACAATCTAGCTTTGTAACCTCTTGAAGCCTCGGACCTGTGACA 746
Db 626 TGTGTTACAGCCGGACAATCTAGCTTTGTAACCTCTTGAAGCCTCGGAACTGTGAACA 685
Qy 747 TCAGCCAGATGGCTCCGACATGACAGTGTCTTCGACCATGACACCGCACAACTTCGGCT 806
Db 686 TCAGCCAGATGGCTCCGACATGACAGTGTCTTCGACCATGACACCGCACAACTTCGGCT 745
Qy 807 TCCGTTTCTTCTATCTTCACTACAAAGCTCAAGCAAGGAGCTTTCAAGCGAAAGACCT 866
Db 746 TCCGTTTCTTCTATCTTCACTACAAAGCTCAAGCAAGGAGCTTTCAAGCGAAAGACCT 805
Qy 867 GTAAGCGAGGACAACTACAGAGACGACGCTGCTCTTCAAATGTTTCTCCAGGGG 926
Db 806 GTAAGCGAGGACAACTACAGAGATGACGAGCTGCTCTTCAAATGTTTCTCCAGGGG 865
Qy 927 ATTATATAATTGAGCTGTGATGACACTAACCAAGAAAGATGATGATATGCT 986
Db 866 ATTATATAATTGAGCTGTGATGACACTAACCAAGAAAGATGATGATATGCT 925
Qy 987 TAAAGCCAGTGCATCTCCCGTGGGCGCGGCCCATCAGAGCCGTGGCCATCAAGTGCAC 1046
Db 926 TAAAGCCAGTGCATCTCCCGTGGGCGCGGCCCATCAGAGCCGTGGCCATCAAGTGCAC 985
Qy 1047 TGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCGGCAAGCAACAG 1106
Db 986 TGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCGGCAAGCAACAG 1045
Qy 1107 AAAATATATATTCATATTTAGATCAAGAGACTCTGAGTCTTCCACATACACTGCAGCAC 1166
Db 1046 AAAATATATATTCATATTTAGATCAAGAGACTCTGAGTCTTCCACATACACTGCAGCAC 1105
Qy 1167 TCCCAAGAGAGAGGCTCCGGCCGCGCGGAAGGCTTTTCTGCTATTTCCAGTAAAGATG 1226

Db 1106 TCCAGAGAGAGGCTCCGGCCGCGCGAAGGCTCTTTCTGTCTATTCCAGTAAAGATG 1165
QY 1227 GCAGAAATCACATGAATGTCGTCCAGTGTTCGCTTACTTCTCCAGGACTTCTGTGGCT 1286
Db 1166 GCAGAAATCACATGAATGTCGTCCAGTGTTCGCTTACTTCTCCAGGACTTCTGTGGCT 1225
QY 1287 GTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAGGGCAGAGAGAT 1346
Db 1226 GTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAGGGCAGAGAGAT 1285
QY 1347 GGGTCATCCAGAAATCCACGAGTCCAGTTCATCATTTGTGTGTGTTTGTTCAAAGGTATGA 1406
Db 1286 GGGTCATCCAGAAATCCACGAGTCCAGTTCATCATTTGTGTGTGTTTGTTCAAAGGTATGA 1345
QY 1407 AGTACTTGTGACAAAGAGAACTACAAACACAAAGAGGTCGCGAGGCTCGGGAAG 1466
Db 1346 AGTACTTGTGACAAAGAGAACTACAAACACAAAGAGGTCGCGAGGCTCGGGAAG 1405
QY 1467 GAGAGCTCTTCTGTGTGGCGGTGTTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAGCAGA 1526
Db 1406 GAGAGCTCTTCTGTGTGGCGGTGTTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAGCAGA 1465
QY 1527 GTTCGTCCGGCGCTCAGCAAGTTTATCCGCTCTACTTTGATTATTTCTCGGAGGAG 1586
Db 1466 GTTCGTCCGGCGCTCAGCAAGTTTATCCGCTCTACTTTGATTATTTCTCGGAGGAG 1525
QY 1587 AGTCCCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCTCAGC 1646
Db 1526 AGTCCCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCTCAGC 1585
QY 1647 TCTGTTCCCACTTGCACCTCCGAGACACGGCTCCAGGAGCGGGCGAGCACAGCGAC 1706
Db 1586 TCTGTTCCCACTTGCACCTCCGAGACACGGCTCCAGGAGCGGGCGAGCACAGCGAC 1645
QY 1707 AGGGCAGCAGAGAACTACTTCCGAGCAAGTCAAGCCGCTCTTATACGTCCGCAATTT 1766
Db 1646 AGGGCAGCAGAGAACTACTTCCGAGCAAGTCAAGCCGCTCTTATACGTCCGCAATTT 1705
QY 1767 GCACATGACCAAGTTTATGAGGAGCGGAGCTGTTTCCGAAAGCAGTTCGTTCCCT 1826
Db 1706 GCACATGACCAAGTTTATGAGGAGCGGAGCTGTTTCCGAAAGCAGTTCGTTCCCT 1765
QY 1827 TCCATCTCTCTCCTACCTGCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTGG 1886
Db 1766 TCCATCTCTCTCCTACCTGCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTGG 1825
QY 1887 TTTTAAATGATGTATGTGCAAAACAGGCGCTGAGAGTCACTTTCCTTAAAGGTAGAG 1946
Db 1826 TTTTAAATGATGTATGTGCAAAACAGGCGCTGAGAGTCACTTTCCTTAAAGGTAGAG 1885
QY 1947 CGGCTGTTCTGGGGCAACCGGACAGCCGACTCCCGACGAGAGTCAAGTGGGGCC 2006
Db 1886 CGGCTGTTCTGGGGCAACCGGACAGCCGACTCCCGACGAGAGTCAAGTGGGGCC 1945
QY 2007 TGGACCAAGAGCGGAGGCGCGCTGCTTACCGTACGCGCGCTTGCACACCCCTGC 2066
Db 1946 TGGACCAAGAGCGGAGGCGCGCTGCTTACCGTACGCGCGCTTGCACACCCCTGC 2005
QY 2067 TGCACACGTTGAAGCGGAGCGCTTCGAGACATGCCGGGACTCAGGCACTATGACT 2126
Db 2006 TGCACACGTTGAAGCGGAGCGCTTCGAGACATGCCGGGACTCAGGCACTATGACT 2065
QY 2127 CGTCTGTGCTCATCCGAGCTGTCTTCCACTGATGAGGACTCTCGAGGACCA 2186
Db 2066 CGTCTGTGCTCATCCGAGCTGTCTTCCACTGATGAGGACTCTCGAGGACCA 2125
QY 2187 CAGAAACGCTTCTCCCTGACGAGAGCGTGTCTCTTCCAGGCTGGGTGAGGAGAAC 2246
Db 2126 CAGAAACGCTTCTCCCTGACGAGAGCGTGTCTCTTCCAGGCTGGGTGAGGAGAAC 2185
QY 2247 CTCCTGCCCTTCTCCAAAGCTCTCTCTTCTGGGTCAAGAGCAGATCTTGGTTGCC 2306
Db 2186 CTCCTGCCCTTCTCCAAAGCTCTCTCTTCTGGGTCAAGAGCAGATCTTGGTTGCC 2245

QY 2307 GCAGCTACACTGATGAATCCACGCGTCCGCGCTTTGTAAACAAACGAAAGAGTCTAAG 2366
Db 2246 GCAGCTACACTGATGAATCCACGCGTCCGCGCTTTGTAAACAAACGAAAGAGTCTAAG 2305
QY 2367 CATTCGCCACTTTAGCTG 2383
Db 2306 CATTCGCCACTTTAGCTG 2322

RESULT 10
US-10-749-144-9
; Sequence 9, Application US/10749144
; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)..(2283)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (118)..()
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
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; OTHER INFORMATION: unknown amino
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; LOCATION: (442)..(442)
; OTHER INFORMATION: unknown amino
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; NAME/KEY: misc_feature
; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
US-10-749-144-9

Query Match 93.1%; Score 2218.6; DB 19; Length 2786;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2292; Conservative 0; Mismatches 20; Indels 45; Gaps 2;
QY 27 CTGGCCAGCGCGCGCGCGCGAGAAACGCGCTTGGCTGGCGGAGCGCACGGCCA 86
Db 11 CGGGCCAGCAGCGCGCGCGCGCGAGAAACGCGCTTGGCTGGCGGAGCGCACGGCCA 70
QY 87 TGGCCCGCTGGGTGCGAGCTCTGCTCGGTCTCTTTTACGGTCAACGCGCTCAACGGCT 146

[illegible]

Db	1106	TCCCAAGAGAGAGGCTCCGGCCGGCGGCGAAGGTCTTTCTCTCTATATCCAGTAAGAATG	1165
Qy	1227	GCCAGAATCACATGAATGTGTCAGAGTGTTCGGCCTACTTCTCCAGGACTTCTGTGGCT	1286
Db	1166	GCCAGNATCANATGAATGTGTCAGAGTGTTCGGCCTACTTCTCCAGGACTTCTGTGGCT	1225
Qy	1287	GTGAGGTGGCTCTGCACTGTGCGGAAGACTTTCAGCCCTCTGTAGAGAAGGCGCAGAGAAT	1346
Db	1256	GTGAGGTGGCTCTGACACTGTGGGAAGACTTTCAGCCCTCTGTAGAGAAGGCGCAGAGAAT	1285
Qy	1347	GGGTCAATCCAGNAGATCCACGAGTCCAGGTCATCATTTGTTGGTTCCTCCAAAGGTATGA	1406
Db	1286	GGGTCAATCCAGNAGATCCACGAGTCCAGGTCATCATTTGTTGGTTCCTCCAAAGGTATGA	1345
Qy	1407	AGTACTTTGTGCAAGAAGAACTACAAACACAAAGGAGTGGCCCGAGGCTCCGGGGAAG	1466
Db	1346	AGTACTTTGTGCAAGAAGAACTACAAACACAAAGGAGTGGCCCGAGGCTCCGGGGAAG	1405
Qy	1467	GAGAGCTCTTCTGTGTGGCGGTGTGAGCCATTTGCCGAAAAGTCCGCCAGGCCAAAGCAGA	1526
Db	1406	GAGAGCTCTTCTGTGTGGCGGTGTGAGCCATTTGCCGAAAAGTCCGCCAGGCCAAAGCAGA	1465
Qy	1527	GTTTGGTCCGGCGGCTCAGCAAGTTTATCGCCGTCTACTTGAATATTCTCTCGAGGGAG	1586
Db	1466	GTTTGGTCCGGCGGCTCAGCAAGTTTATCGCCGTCTACTTGAATATTCTCTCGAGGGAG	1525
Qy	1587	ACGTCCCCTGGTATCTAGACCTGAGTACCAGATACAGACTCATGAGCAATCTTCTCTCAGC	1646
Db	1526	ACGTCCCCTGGTATCTAGACCTGAGTACCAGATACAGACTCATGAGCAATCTTCTCTCAGC	1585
Qy	1647	TCTGTTTCCCATTTGCACTCCCGAGACCAGGCTTCCAGAGCCGGGGCAGCACACGGCAC	1706
Db	1586	TCTGTTTCCCATTTGCACTCCCGAGACCAGGCTTCCAGAGCCGGGGCAGCACACGGCAC	1645
Qy	1707	AGGGCAGCAGAAAGAACTACTTTCGGAGCAAGTCAGGCCGGTCCCTTAGCTGCCCAATTT	1766
Db	1646	AGGGCAGCAGAAAGAACTACTTTCGGAGCAAGTCAGGCCGGTCCCTTAGCTGCCCAATTT	1705
Qy	1767	GCAACATGCACCAAGTTTATTGACGAGGAGCCCGACTGGTTTCGAAAAGCAGTTCGTTCCCT	1826
Db	1706	GCAACATGCACCAAGTTTATTGACGAGGAGCCCGACTGGTTTCGAAAAGCAGTTCGTTCCCT	1765
Qy	1827	TCCATCTCTCTCACTCGCTACCCGGAGCCAGTCTTGAGAAATTTGATTCGGGCTTGG	1886
Db	1766	TCCATCTCTCTCACTCGCTACCCGGAGCCAGTCTTGAGAAATTTGATTCGGGCTTGG	1825
Qy	1887	TTTTAAATGATGTCAATGTGCAAAACCAAGGCTGTGAGAGTCACTTTCGCTAAAGGTAGAGG	1946
Db	1826	TTTTAAATGATGTCAATGTGCAAAACCAAGGCTGTGAGAGTCACTTTCGCTAAAGGTAGAGG	1885
Qy	1947	CGGCTGTTCTTTGGGCGCAACCGGACACAGCGACTCCACGACACGAGAGTCAGCATGGGGGCC	2006
Db	1886	CGGCTGTTCTTTGGGCGCAACCGGACACAGCGACTCCACGACACGAGAGTCAGCATGGGGGCC	1945
Qy	2007	TGGACCAAGACGGGAGGCGCGGCTTGCCTTTGACGGTAGCGCCGCTGCAACCCCTGC	2066
Db	1946	TGGACCAAGACGGGAGGCGCGGCTTGCCTTTGACGGTAGCGCCGCTGCAACCCCTGC	2005
Qy	2067	TGCACACGGTGAAGCGCGCAGCCCTCGGACATGCCCGGGGACTCAGGCACTATGACT	2126
Db	2006	TGCACACGGTGAAGCGCGCAGCCCTCGGACATGCCCGGGGACTCAGGCACTATGACT	2065
Qy	2127	CGTCTGTCCTCATCTCGAGCTGTCTTCGCCACTGATGAAGAGACTTCGACGAGCCAGA	2186
Db	2066	CGTCTGTCCTCATCTCGAGCTGTCTTCGCCACTGATGAAGAGACTTCGACGAGCCAGA	2125
Qy	2187	CAGAAACGTCTTCCCTTGACGGAGCGGTCTCTCTTTCAGGCCCTGGGTGAGGAGAAC	2246
Db	2126	CAGAAACGTCTTCCCTTGACGGAGCGGTCTCTCTTTCAGGCCCTGGGTGAGGAGAAC	2185
Qy	2247	CTCTGCGCCTTCTTCCAAAGCTCTCTCTTCTTGGGTCATGCAAAGCAGATCTTGTTGCC	2306
Db	2186	CTCTGCGCCTTCTTCCAAAGCTCTCTCTTCTTGGGTCATGCAAAGCAGATCTTGTTGCC	2245

		; SEQ ID NO 1		Query Match		93.0%; Score 2215.4; DB 14; Length 3083;	
		; LENGTH: 3083		Best Local Similarity		97.9%; Pred. No. 0;	
		; TYPE: DNA		Matches 2271; Conservative		0; Mismatches 6; Indels 42; Gaps 1;	
		; ORGANISM: Homo sapiens					
		; FEATURE:					
		; NAME/KEY: CDS					
		; LOCATION: (22)..(2235)					
		US-10-216-156-1					
Qy	65	TGGCTGGGCGAGCGCACGGCCATGGCCCGTGGCTGCGAGCTCTGCTCCGCTCTTCTTTAAG	124				
Db	1	TGGCTGGGCGAGCGCACGGCCATGGCCCGTGGCTGCGAGCTCTGCTCCGCTCTTCTTTAAG	60				
Qy	125	GTCAACGCTGCCTCAACGGCTCGCAGCTGCTGTGCGCGCTGCGGGTCCGGCGCGCG	184				
Db	61	GTCAACGCTGCCTCAACGGCTCGCAGCTGCTGTGCGCGCTGCGGGTCCGGCGCGCG	120				
Qy	185	CGGGCGCGCAGACCTGTGGCTGAGGATGAAGCGGCTGCCCGACCCCGCTTTGTGTT	244				
Db	121	TGGGCGGTGCAACCTGTGGCTGGAG-----	146				
Qy	245	GCTAATGAGGGAGTGGGSCCAGCCAGCAGAAACAGTGGGCTGTACAAATCACCTTCAAA	304				
Db	147	-----GGAGTGGGSCCAGCCAGCAGAAACAGTGGGCTGTACAAATCACCTTCAAA	198				
Qy	305	TATGACAATTGTACACCTACTTGAATCCAGTGGGGAAGCATGTGATGTGTCAGCCCGAG	364				
Db	199	TATGACAATTGTACACCTACTTGAATCCAGTGGGGAAGCATGTGATGTGTCAGCCCGAG	258				
Qy	365	AATATCACCATCAGCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAATTTCTTTGTTCC	424				
Db	259	AATATCACCATCAGCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAATTTCTTTGTTCC	318				
Qy	425	CCAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCCGGGTAACTACTGGAGGAGCTGAAG	484				
Db	319	CCAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCCGGGTAACTACTGGAGGAGCTGAAG	378				
Qy	485	TCGGAGGGAAGACAGTGCACAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGC	544				
Db	379	TCGGAGGGAAGACAGTGCACAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGC	438				
Qy	545	TTCAAAAGAACTGGAATCGAATCTCAACCTTCTCTGAAATATGAATTTGAAACGGATTAT	604				
Db	439	TTCAAAAGAACTGGAATCGAATCTCAACCTTCTCTGAAATATGAATTTGAAACGGATTAT	498				
Qy	605	TTCTGTAAGGTTGTCCCTTTTCTTCATTAAACGAAAGCAATTAACCCCTTTCTTC	664				
Db	499	TTCTGTAAGGTTGTCCCTTTTCTTCATTAAACGAAAGCAATTAACCCCTTTCTTC	558				
Qy	665	TTTAGAACCCGAGCTGTGACCTGTGTGTTACAGCCGGAACAATCTAGCTTGTAAACCCCTTC	724				
Db	559	TTTAGAACCCGAGCTGTGACCTGTGTGTTACAGCCGGAACAATCTAGCTTGTAAACCCCTTC	618				
Qy	725	TGGAAGCCTCGGAACCTGGAACATCAGCCAGCATGGCTCGGACATGCGAGGTGCTTTGAC	784				
Db	619	TGGAAGCCTCGGAACCTGGAACATCAGCCAGCATGGCTCGGACATGCGAGGTGCTTTGAC	678				
Qy	785	CATGCACCGCAACTTCGGCTTCGGTTTCTTCTATCTTCACTCAAGCTCAAGCAGCAA	844				
Db	679	CACGCACCGCAACTTCGGCTTCGGTTTCTTCTATCTTCACTCAAGCTCAAGCAGCAA	738				
Qy	845	GGACCTTTCAAGCGAAGAACCTGTAAAGCAGGAGCAAACTACAGAGACGACAGCTGCCTC	904				
Db	739	GGACCTTTCAAGCGAAGAACCTGTAAAGCAGGAGCAAACTACAGAGACGACAGCTGCCTC	798				
Qy	905	CTTCAAAATGTTTCTCCAGGGGAATTATATAATTGAGCTGGTGGATGACACTTAAACAACA	964				
Db	799	CTTCAAAATGTTTCTCCAGGGGAATTATATAATTGAGCTGGTGGATGACACTTAAACAACA	858				

Db 1939 AGCGCGCCCTGCAACCCCTGCTGCACACGGTGAAGCGCGCAGCCCTCGGACATGCGG 1998
Qy 2105 CGGAGCTCAGGACATATGACTCGTCTGCGCTCATCCGAGCTGTCTCTGCCACTGATG 2164
Db 1999 CGGAGCTCAGGACATATGACTCGTCTGCGCTCATCCGAGCTGTCTCTGCCACTGATG 2058
Qy 2165 GAAGGACTCTCGACGGACAGACAGAAACGCTTCCCTCGAGGAGAGCGTGTCTCTCTCT 2224
Db 2059 GAAGGACTCTCGACGGACAGACAGAAACGCTTCCCTCGAGGAGAGCGTGTCTCTCTCT 2118
Qy 2225 TCAGGCTGGGTGAGAGAAACCTCTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2284
Db 2119 TCAGGCTGGGTGAGAGAAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2178
Qy 2285 TGCAAGCAGATCTTGGTGGCGGAGCTACACTGATGAATCCAGCGGTGCGCCCTTTG 2344
Db 2179 TGCAAGCAGATCTTGGTGGCGGAGCTACACTGATGAATCCAGCGGTGCGCCCTTTG 2238
Qy 2345 TAACAAACGAAAGAGTCTAAGCATTGGCACTTTAGCTG 2383
Db 2239 TAACAAACGAAAGAGTCTAAGCATTGGCACTTTAGCTG 2277

RESULT 14

US-10-616-788-1

; Sequence 1, Application US/10616788
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; CURRENT APPLICATION NUMBER: US/10/616,788
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 09/809,567
; FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(2235)

US-10-616-788-1

Query Match 93.0%; Score 2215.4; DB 18; Length 3083;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2271; Conservative 0; Mismatches 6; Indels 42; Gaps 1;
Qy 65 TGGCTGGGCGAGCGACGCGCATGCGCGTGGCTGCGAGCTGTCTCGTCTTTTACG 124
Db 1 TGGCTGGGCGAGCGACGCGCATGCGCGTGGCTGCGAGCTGTCTCGTCTTTTACG 60
Qy 125 GTCAACGCTGCTCTCAACGGCTCGCAGCTGGCTGTGGCGCTGGCGGGTCCGCGCGCGG 184
Db 61 GTCAACGCTGCTCTCAACGGCTCGCAGCTGGCTGTGGCGCTGGCGGGTCCGCGCGCGG 120
Qy 185 CGGCGCGCGACACCTGTGGCTGGAGGATGAAGCGGCTGCGCGACCCCGGCTTTGTGTT 244
Db 121 TGGGCGGTGACACCTGTGGCTGGAG----- 146
Qy 245 GCTAATAGGGAGTGGGCGACGACAGAAACAGTGGCTGTACACATCACCTTCAA 304
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; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SRF Molecule and Uses
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; TITLE OF INVENTION: Therefor
; FILE REFERENCE: MPI03-071P1RM
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; PRIOR FILING DATE: 2004-05-07
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; PRIOR FILING DATE: 2003-05-08
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ALIGNMENTS

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; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2344)
US-09-912-157-1

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Best Local Similarity 100.0%; Pred. No. 4.3e-35;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICANT: Priesnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
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; SEQ ID NO 4
; LENGTH: 2383
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; ORGANISM: Homo sapiens
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; NAME/KEY: CDS
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US-09-912-157-4

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; Publication No. US20040077052A1
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; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
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; Publication No. US20040077052A1
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; APPLICANT: Preenell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
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US-10-717-282-4

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; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23

RESULT IS
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 ; Publication NO. US20040197306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Daniel M.
 ; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
 ; FILE REFERENCE: DX01170K1

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Title: US-10-717-282-2

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Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4013	100.0	753	Sequence 2, Appli
3	4003	99.8	753	US-10-717-282-2
4	4003	99.8	753	Sequence 5, Appli
5	3925	97.8	739	US-10-717-282-5
6	3925	97.8	739	Sequence 8, Appli
7	3915	97.6	739	US-10-717-282-8
8	3915	97.6	739	Sequence 2, Appli
9	3905	97.3	739	US-10-842-006-2
10	3901	97.2	738	US-10-608-449-2
11	3901	97.2	738	US-09-809-567-2

12	3901	97.2	738	15	US-10-616-788-2	Sequence 2, Appli
13	3835.5	95.6	738	10	US-09-863-818A-10	Sequence 10, Appl
14	3835.5	95.6	738	16	US-10-749-144-10	Sequence 10, Appl
15	3835.5	95.6	738	17	US-10-924-667-10	Sequence 10, Appl
16	3708	92.4	728	15	US-10-104-047-3399	Sequence 3399, Ap
17	3703	92.3	728	9	US-09-874-503-18	Sequence 18, Appl
18	3703	92.3	728	10	US-09-816-744-18	Sequence 18, Appl
19	3703	92.3	728	10	US-09-747-259-18	Sequence 18, Appl
20	3703	92.3	728	10	US-09-908-827-18	Sequence 18, Appl
21	3703	92.3	728	13	US-10-000-157-18	Sequence 18, Appl
22	3703	92.3	728	14	US-10-410-927-18	Sequence 18, Appl
23	3703	92.3	728	14	US-10-410-374-18	Sequence 18, Appl
24	3703	92.3	728	14	US-10-410-552-18	Sequence 18, Appl
25	3703	92.3	728	15	US-10-458-442-18	Sequence 18, Appl
26	3703	92.3	728	15	US-10-408-385-18	Sequence 18, Appl
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32	1337	33.3	296	15	US-10-616-788-19	Sequence 19, Appl
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36	312	7.8	866	9	US-09-778-971-9	Sequence 9, Appli
37	312	7.8	866	13	US-10-033-522-1	Sequence 1, Appli
38	312	7.8	866	14	US-10-207-655-107	Sequence 107, App
39	312	7.8	866	16	US-10-742-161-10	Sequence 10, Appl
40	312	7.8	866	16	US-10-742-372-10	Sequence 10, Appl
41	312	7.8	866	16	US-10-646-308-4	Sequence 4, Appli
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43	306	7.6	864	16	US-10-742-161-2	Sequence 2, Appli
44	306	7.6	864	16	US-10-742-372-2	Sequence 2, Appli
45	232.5	5.8	207	10	US-09-863-818A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-912-157-2
; Sequence 2, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-2

Query Match 100.0%; Score 4013; DB 9; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MAPWLQCSVFTVNACLNGSOLAAGSGRARGADTCGWRMKAAARPRLCVANEVGP 60
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Qy 421 WVIQKHESQFIIVVCSKGMKYFVDKKNYKHGGSGKGELFLVAVSAIAEKLROAKQ 480
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RESULT 2

US-10-717-282-2

; Sequence 2, Application US/10717282

; Publication No. US20040077052A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/10/717,282

; CURRENT FILING DATE: 2003-11-19

; PRIOR APPLICATION NUMBER: US/09/912,157

; PRIOR FILING DATE: 2001-07-24

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-717-282-2

Query Match 100.0%; Score 4013; DB 15; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-912-157-5

; Sequence 5, Application US/09912157

; Patent No. US20020165348A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-157-5

Query Match 99.8%; Score 4003; DB 9; Length 753;
Best Local Similarity 99.7%; Pred. No. 0;
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RESULT 4

US-10-717-282-5

; Sequence 5, Application US/10717282

; Publication No. US20040077052A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/10/717,282

; CURRENT FILING DATE: 2003-11-19

; PRIOR APPLICATION NUMBER: US/09/912,157

; PRIOR FILING DATE: 2001-07-24

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-717-282-5

Query Match 99.8%; Score 4003; DB 15; Length 753;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 61 ASRNSGLNYITFKYDNCTTYLNPVGHVIAAQNITISQYACHQVAVTILWSPGALGIE 120
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Db 121 FLKGRVILBELKSEGRQCOQLILKDPKQLNSSFRTGMSQPFNLKMFETDYFKVVPF 180
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Db 481 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLROAKQ 540
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Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAALQPL 660
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RESULT 5

US-09-912-157-8

; Sequence 8, Application US/09912157

; Patent No. US20020165348A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-8

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Best Local Similarity 98.1%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

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Db 107 FLKGFVRVILEELKSEGRCCQQLILKDPKQLNSSFKRTGMESQPLNMKFETDYFVKVVPF 166

Qy 181 PSIKNESNYHPPFRTRACDLLLPDLNACKPFWKPRNLNISQHGSDMQVSFDHAPNFG 240
Db 167 PSIKNESNYHPPFRTRACDLLLPDLNACKPFWKPRNLNISQHGSDMQVSFDHAPNFG 226

Qy 241 FRFFYLHYKLKHEGPFKRTCKQBOETTETSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
Db 227 FRFFYLHYKLKHEGPFKRTCKQBOETTETSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286

Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTAA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTAA 346

Qy 361 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406

Qy 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 480
Db 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 466

Qy 481 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 540
Db 467 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 526

Qy 541 QGSRNRYFRSKGSLYVAICNMHQFIDEEPDMFEKQFVPPHPPPLRYREPVLKFPDGL 600
Db 527 QGSRNRYFRSKGSLYVAICNMHQFIDEEPDMFEKQFVPPHPPPLRYREPVLKFPDGL 586

Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQGEARPALDGSAAALQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQGEARPALDGSAAALQPL 646

Qy 661 LHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMEGLSTDQETSSLTESVSSSGLGEE 720
Db 647 LHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMEGLSTDQETSSLTESVSSSGLGEE 706

Qy 721 PPALPSKLLSGSGCKADLGCRSYTDELHAVAPL 753
Db 707 PPALPSKLLSGSGCKADLGCRSYTDELHAVAPL 739

RESULT 6
US-10-717-282-8
; Sequence 8, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/10717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-282-8

Query Match      97.8%; Score 3925; DB 15; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFFTVNACLSQSLAAAGGSGRAGADTCGWRKMAAARPLCLVANEGVGP 60
Db 1 MAPWLQCSVFFTVNACLSQSLAAAGGSGRAGADTCGWR-----GVGP 46

Qy 61 ASRNSGLYNTTFKYDNCCTYLNPGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTTFKYDNCCTYLNPGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 106

Qy 121 FLKGFVRVILEELKSEGRCCQQLILKDPKQLNSSFKRTGMESQPLNMKFETDYFVKVVPF 180
Db 107 FLKGFVRVILEELKSEGRCCQQLILKDPKQLNSSFKRTGMESQPLNMKFETDYFVKVVPF 166

Qy 181 PSIKNESNYHPPFRTRACDLLLPDLNACKPFWKPRNLNISQHGSDMQVSFDHAPNFG 240
Db 167 PSIKNESNYHPPFRTRACDLLLPDLNACKPFWKPRNLNISQHGSDMQVSFDHAPNFG 226

Qy 241 FRFFYLHYKLKHEGPFKRTCKQBOETTETSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
Db 227 FRFFYLHYKLKHEGPFKRTCKQBOETTETSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286

Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTAA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTAA 346

Qy 361 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406

Qy 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 480
Db 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 466

Qy 481 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 540
Db 467 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 526

Qy 541 QGSRNRYFRSKGSLYVAICNMHQFIDEEPDMFEKQFVPPHPPPLRYREPVLKFPDGL 600
Db 527 QGSRNRYFRSKGSLYVAICNMHQFIDEEPDMFEKQFVPPHPPPLRYREPVLKFPDGL 586

Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQGEARPALDGSAAALQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQGEARPALDGSAAALQPL 646

Qy 661 LHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMEGLSTDQETSSLTESVSSSGLGEE 720
Db 647 LHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMEGLSTDQETSSLTESVSSSGLGEE 706

Qy 721 PPALPSKLLSGSGCKADLGCRSYTDELHAVAPL 753
Db 707 PPALPSKLLSGSGCKADLGCRSYTDELHAVAPL 739

RESULT 7
US-10-842-006-2
; Sequence 2, Application US/10842006
; Publication No. US20040235104A1
```

GENERAL INFORMATION:

APPLICANT: Yang, Ruy-Bing
TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
FILE REFERENCE: MPI03-071PIRM
CURRENT APPLICATION NUMBER: US/10/842,006
PRIOR FILING DATE: 2004-05-07
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 739
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-842-006-2

Query Match 97.6%; Score 3915; DB 16; Length 739;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 737; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
Qy 1 MAPWLQCSVFFTVNACINGSQLA VAAAGSGRARGADTCGRMKAAARPRLCVANEVGP 60
Db 1 MAPWLQCSVFFTVNACINGSQLA VAAAGSGRARGADTCGRMKAAARPRLCVANEVGP 46
61 ASRNSGLYNTFFKYDNCCTTYLNPVGHVIA DAQNITISQVACHDQVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTFFKYDNCCTTYLNPVGHVIA DAQNITISQVACHDQVAVTILWSPGALGIE 106
121 FLKGFVRVILELSEKSGRQCQQLILKDPKQLNSSFKRTGMESQPLNMFETDYFVKVVPF 180
Db 107 FLKGFVRVILELSEKSGRQCQQLILKDPKQLNSSFKRTGMESQPLNMFETDYFVKVVPF 166
181 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 240
Db 167 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 226
241 FRPFYLYLKHGEPFRKTKCQBOTETTSCLLQNVSPGDYIILELVDNTTTRKVMHYA 300
Db 227 FRPFYLYLKHGEPFRKTKCQBOTETTSCLLQNVSPGDYIILELVDNTTTRKVMHYA 286
301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346
361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406
421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 480
Db 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 466
481 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 540
Db 467 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 526
541 QGSRNRYFRSKGSLYVAICNMHQFIDEEPDWFEKQVPPHPPPLRYRPEVLEKFDGSL 600
Db 527 QGSRNRYFRSKGSLYVAICNMHQFIDEEPDWFEKQVPPHPPPLRYRPEVLEKFDGSL 586
601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQPL 646
661 LHTVAGSPSPDPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSSGLGEE 720
Db 647 LHTVAGSPSPDPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSSGLGEE 706
721 PPALPSKLLSSGCKADLGCRSYTDDELHAVA PL 753
707 PPALPSKLLSSGCKADLGCRSYTDDELHAVA PL 739

RESULT 8

US-10-608-449-2
Sequence 2, Application US/10608449
Publication No. US20040265834A1
GENERAL INFORMATION:
APPLICANT: Tsinghua University
TITLE OF INVENTION: Human interleukin-17 Receptor Like Molecule
FILE REFERENCE: I2003269C-US
CURRENT APPLICATION NUMBER: US/10/608,449
CURRENT FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 739
TYPE: PRT
ORGANISM: Homo sapiens
US-10-608-449-2

Query Match 97.6%; Score 3915; DB 16; Length 739;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 737; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
Qy 1 MAPWLQCSVFFTVNACINGSQLA VAAAGSGRARGADTCGRMKAAARPRLCVANEVGP 60
Db 1 MAPWLQCSVFFTVNACINGSQLA VAAAGSGRARGADTCGRMKAAARPRLCVANEVGP 46
61 ASRNSGLYNTFFKYDNCCTTYLNPVGHVIA DAQNITISQVACHDQVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTFFKYDNCCTTYLNPVGHVIA DAQNITISQVACHDQVAVTILWSPGALGIE 106
121 FLKGFVRVILELSEKSGRQCQQLILKDPKQLNSSFKRTGMESQPLNMFETDYFVKVVPF 180
Db 107 FLKGFVRVILELSEKSGRQCQQLILKDPKQLNSSFKRTGMESQPLNMFETDYFVKVVPF 166
181 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 240
Db 167 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 226
241 FRPFYLYLKHGEPFRKTKCQBOTETTSCLLQNVSPGDYIILELVDNTTTRKVMHYA 300
Db 227 FRPFYLYLKHGEPFRKTKCQBOTETTSCLLQNVSPGDYIILELVDNTTTRKVMHYA 286
301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346
361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406
421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 480
Db 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 466
481 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 540
Db 467 SSSAALSXFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 526
541 QGSRNRYFRSKGSLYVAICNMHQFIDEEPDWFEKQVPPHPPPLRYRPEVLEKFDGSL 600
Db 527 QGSRNRYFRSKGSLYVAICNMHQFIDEEPDWFEKQVPPHPPPLRYRPEVLEKFDGSL 586
601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQPL 646
661 LHTVAGSPSPDPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSSGLGEE 720
Db 647 LHTVAGSPSPDPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSSGLGEE 706
721 PPALPSKLLSSGCKADLGCRSYTDDELHAVA PL 753
PPALPSKLLSSGCKADLGCRSYTDDELHAVA PL 739

Db 707 PPALPSKLLSSGCKADLGRSYTDELHVAAPL 739

RESULT 9
US-10-842-006-4
; Sequence 4, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruy-Bing
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses Therefor
; FILE REFERENCE: MPI03-07IPRM
; CURRENT APPLICATION NUMBER: US/10/842,006
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-006-4

Query Match 97.3%; Score 3905; DB 16; Length 739;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 735; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFFTVNACLSQLAVAAGSGRGARADTCGRWKAAARPRLCVANEGVGP 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MAPWLQCSVFFTVNACLSQLAVAAGSGRAWGYDTGWR-----GVGP 46
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 ASNSGLYNTFKYDNCCTTYLPVGKHVIADAQNITISQYACHDOAVATILWSPGALGIE 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 47 ASNSGLYNTFKYDNCCTTYLPVGKHVIADAQNITISQYACHDOAVATILWSPGALGIE 106
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 FLKGFVRVILEELKSEGRQCQQLIKDPKQLNSSFKRTGMESOPFLNMKFETDYFKVVVPF 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 107 FLKGFVRVILEELKSEGRQCQQLIKDPKQLNSSFKRTGMESOPFLNMKFETDYFKVVVPF 166
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 PSIKNESNYHPFFRTRACDLLLOPNLACKFPWKPRNLINISQHSDMQVSFDHAPHNFG 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 167 PSIKNESNYHPFFRTRACDLLLOPNLACKFPWKPRNLINISQHSDMQVSFDHAPHNFG 226
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 241 FRFYLYHLKHGEPFRKTCKOEQTETTSCLLQNVSPGDVII ELVDVTNTRKMHYA 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 227 FRFYLYHLKHGEPFRKTCKOEQTETTSCLLQNVSPGDVII ELVDVTNTRKMHYA 286
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 301 LKPVHSWPAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEESESSTYTAA 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 LKPVHSWPAGPIRAMAITVPLVVISAFATLFTVMCRKKQENIYSHLDEESESSTYTAA 346
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 361 LPRLRLRPKPVFLCYSSKDQQNHMNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 347 LPRLRLRPKPVFLCYSSKDQQNHMNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 406
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 421 WVIQTHESOFIIIVCCKGMKYFVDKNYKHGGGSGKGELFLVAVSAIAEKLRQAQ 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 467 SSAAALSKEFTAVFDYSCEGDVPGILDSTKYRLMDNLPLQCSHLHSRDHGLQEPPQHTR 526
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 541 QGSRRNYFRSKSRSLYVAICNNHQFIIDEEPWFKEQFVFPFPPPLRYREPVLKFDSSL 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 527 QGSRRNYFRSKSRSLYVAICNNHQFIIDEEPWFKEQFVFPFPPPLRYREPVLKFDSSL 586
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 601 VLNDVMCKPGEPSDFCLKVBAALVIGATGPADSQHSCHGGLDQDGEARPALDGSAAOLPL 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 587 VLNDVMCKPGEPSDFCLKVBAALVIGATGPADSQHSCHGGLDQDGEARPALDGSAAOLPL 646
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

561 IHTVKAGSPSMDPDGSIYDVSSVPSSELSPLMEGLSTDQITSETSVSSSSGGLGEE 720

us-10-717-282-2.rapb

QY	481	SSSAALSKFIATVYFDYSCEGDVPGILDLSTKYRLMDNLPOLCSHLHSDHGLQBPQGHTR	544
DB	467	SSSAALSKFIATVYFDYSCEGDVPGILDLSTKYRLMDNLPOLCSHLHSDHGLQBPQGHTR	526
QY	541	QGSRRNYFRSKSRSLVAICNNHQFTDERPDPFEKQFVPPHPPLRYREPVLKFDGSL	600
DB	527	QGSRRNYFRSKSRSLVAICNNHQFTDERPDPFEKQFVPPHPPLRYREPVLKFDGSL	586
QY	601	VLNDVMCKPGESDFCLKVEAAVLGATGPADSQHESQHGGGLDQGEARPALDGSAAQLPL	660
DB	587	VLNDVMCKPGESDFCLKVEAPVLGATGPADSQHESQHGGGLDQGEARPALDGSAAQLPL	646
QY	661	LHTVKAGSPDMPRDSGIYDSSVPSSELSIPLMEGLSTDQTETSSLTBSVSSSSGLGHEE	720
DB	647	LHTVKAGSPDMPRDSGIYDSSVPSSELSIPLMEGLSTDQTETSSLTBSVSSSSGLGHEE	706
QY	721	PPALPSKLLSSGCKADLGCRSYTDDELHAVAP	752
DB	707	PPALPSKLLSSGCKADLGCRSYTDDELHAVAP	738
RESULT 12			
US-10-616-788-2			
; Sequence 2, Application US/10616788			
; Publication No. US20040048338A1			
; GENERAL INFORMATION:			
; APPLICANT: Jing, Shuqian			
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof			
; FILE REFERENCE: 01017/39525			
; CURRENT APPLICATION NUMBER: US/10/616,788			
; CURRENT FILING DATE: 2003-07-10			
; PRIOR APPLICATION NUMBER: 09/809,567			
; PRIOR FILING DATE: 2001-03-15			
; PRIOR APPLICATION NUMBER: 09/724,460			
; PRIOR FILING DATE: 2000-11-28			
; PRIOR APPLICATION NUMBER: 60/189,816			
; PRIOR FILING DATE: 2000-03-16			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 2			
; LENGTH: 738			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-616-788-2			
Query Match 97.2%; Score 3901; DB 15; Length 738;			
Best Local Similarity 97.6%; Pred. No. 0;			
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1			
QY	1	MAPWLQCLSVFFFTVACINCSQLAAVAGGSGRAGDTCGHRMKAAARPRLCVANEVGP	60
DB	1	MAPWLQCLSVFFFTVACINCSQLAAVAGGSGRAWGVDTCGWR	46
QY	61	ASRNSGLNYITFKYDNCNTTYLNPVGKHVIADAQNITISQYACHDOVAVTILWSPGALGIE	120
DB	47	ASRNSGLNYITFKYDNCNTTYLNPVGKHVIADAQNITISQYACHDOVAVTILWSPGALGIE	106
QY	121	FLKGFRVILBELKSEGRCCQQLILKDPKQLNSSFKRTGMESQFFLNMKPFETDYFVKVVPF	180
DB	107	FLKGFRVILBELKSEGRCCQQLILKDPKQLNSSFKRTGMESQFFLNMKPFETDYFVKVVPF	166
QY	181	PSIKNESNYHPFFPTRACDLLLLQPDNLACKPFWKPRNLNISOHGSMDQVSDFHAPHNFG	240
DB	167	PSIKNESNYHPFFPTRACDLLLLQPDNLACKPFWKPRNLNISOHGSMDQVSDFHAPHNFG	226
QY	241	FRFPYLHYKLKHEGPFPRKCTCKQQTETTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA	300
DB	227	FRFPYLHYKLKHEGPFPRKCTCKQQTETTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA	286
QY	301	LKPVHSPWAGPIRAVAITVPLVWISAPATLFTVMCRKKQOENIYSHLDESSSESSTYTAA	360
DB	287	LKPVHSPWAGPIRAVAITVPLVWISAPATLFTVMCRKKQOENIYSHLDESSSESSTYTAA	346

; Sequence 10, Application US/10749144
; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(26)
; OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109)..(109)
; OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120)..(120)
; OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
; - 10749-144-10
Query Match 95.6%; Score 3835.5; DB 16; Length 738;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 726; Conservative 2; Mismatches 10; Indels 15; Gaps 2;
Qy 1 MAPLQLCSVFTVNAACLSQSLVAAGSGRARGADTCGWRMKAARPRCLCVANEGVGP 60
Db 1 MAPLQLCSVFTVNAACLSQSLVAAGSGRARGADTCGWRMKAARPRCLCVANEGVGP 60
Qy 61 ASRNSGLNITFKYDNCCTYLNPKGVKVIADAQNTISQYACHDOVAVTILWSPGALGIE 120
Db 47 ASRNSGLNITFKYDNCCTYLNPKGVKVIADAQNTISQYACHDOVAVTILWSPGALGIE 106
Qy 121 FLKGRVILELKGEGROCOQLILKDPKOLNSSFKRTGMSQPLNMMKFETDIFVKVVPF 180
Db 107 FLKGRVILELKGEGROCOQLILKDPKOLNSSFKRTGMSQPLNMMKFETDIFVR-USF 165
Qy 181 PSIKNESNYHPPFFRTRACDILLQDNLACPKFPWKPRNLINISQHGSDMQVDFDHPHNF 240
Db 166 SFIKNESNYHPPFFRTRACDILLQDNLACPKFPWKPRNLINISQHGSDMQVDFDHPHNF 225
Qy 241 FRFFYLHYLKHGEPFKRKTCKEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 300
Db 236 FRFFYLHYLKHGEPFKRKTCKEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 285
Qy 301 LKPVHSPWAGPIRAVAITVPLVISAFATLFTVMCKKQENIYSHLDEESSESTYTA 360
Db 286 LKPVHSPWAGPIRAVAITVPLVISAFATLFTVMCKKQENIYSHLDEESSESTYTA 345
Qy 361 LPRRLRPKPVFLCYSSKDGQNMNVVQCFCAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 346 LPRRLRPKPVFLCYSSKDGQNMNVVQCFCAYFLQDFCGCEVALDLWEDFSLCREGORE 405
Qy 421 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKLRQAKQ 480
Db 406 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKLRQAKQ 465

Qy 481 SSSAALSFKFIAYFDYSCBGDVPGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGQTR 540
Db 466 SSSAALSFKFIAYFDYSCBGDVPGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGQTR 525
Qy 541 QGSRNRYFRSKSGSLVAICNMHQFIDEEPDPWEKQFVPPHPPPLRYREPVLKFDGSL 600
Db 526 QGSRNRYFRSKSGSLVAICNMHQFIDEEPDPWEKQFVPPHPPPLRYREPVLKFDGSL 585
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAALDGSAAALQPL 660
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Qy 661 LHTVAGSPDMPRDSGIYDSSVSPSSLSLPLMEGLSTDQTETSSLSLTSVSSSSGLGEE 720
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Qy 721 PPALPSKLLSGSGCKADLGCRSYTDELHVAAPL 753
Db 706 PPALPSKLLSGSGCKADLGCRSYTDELHVAAPL 738
RESULT 15
US-10-924-667-10
; Sequence 10, Application US/10924667
; Publication No. US20050009145A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/10/924,667
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/09/863,818
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or
; OTHER INFORMATION: Leu.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(26)
; OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or
; OTHER INFORMATION: Met.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109)..(109)
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; OTHER INFORMATION: Cys.
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; LOCATION: (120)..(120)
; OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (134)..(134)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
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US-10-924-667-10

Query Match 95.6%; Score 3835.5; DB 17; Length 738;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 726; Conservative 2; Mismatches 10; Indels 15; Gaps 2;
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Db 47 ASRNSGLYNTTFKYDNCCTTYLNPVKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 106
Qy 121 FLKGFVILBELKSEGQCOOLILKDPKOLNSFKRTGMESQPLNMKFETDYEVKVVVF 180
Db 107 FLKGFVILBELKSEGQXQOLILKDPKQXNSFKRTGMESQPLNMKFETDYFVR-LSF 165
Qy 181 PSIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISQHGSDMQVSDFHAPHNFG 240
Db 166 SFIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISQHGSDMQVSDFHAPHNFG 225
Qy 241 FRPFLHYKLKHEGPFKRKTKQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
Db 226 FRPFLHYKLKHEGPFKRKTKQQTETMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 285
Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQQENIYSHLDEESSESSTYAA 360
Db 286 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQQENIYSHLDEESSESSTYAA 345
Qy 361 LPRRLRPRPKVFLCYSSKQGNHNVVQCFCAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 346 LPRRLRPRPKVFLCYSSKQGNHNVVQCFCAYFLQDFCGCEVALDLWEDFSLCREGORE 405
Qy 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLROAKQ 480
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Qy 481 SSSAALSXFIANYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSRDHGLQEPGQHTR 540
Db 466 SSSAALSXFIANYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSRDHGLQEPGQHTR 525
Qy 541 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPDWFEKQFVPPHPPPLRYREPVLKFDGSL 600
Db 526 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPDWFEKQFVPPHPPPLRYREPVLKFDGSL 585
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAALOPL 660
Db 586 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAALOPL 645
Qy 661 LHTVKAGSPDMPRDSGIYDSVSPSSLSLPLMEGLSTDQTETSSLTESVSSSGLGEEE 720

Db 646 LHTVKAGSPDMPRDSGIYDSVSPSSLSLPLMEGLSTDQTETSSLTESVSSSGLGEEE 705
Qy 721 PPALPSKLLSSGSKADLGCRSYTDELHVAAPL 753
Db 706 PPALPSKLLSSGSKADLGCRSYTDELHVAAPL 738
Search completed: August 9, 2005, 11:54:38
Job time : 112.034 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:40:52 ; Search time 103.966 Seconds
(without alignments)
2696.128 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

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Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 39037842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3829	100.0	753	9	US-09-912-157-2
2	3829	100.0	753	15	US-10-717-282-2
3	3819	99.7	753	9	US-09-912-157-5
4	3819	99.7	753	15	US-10-717-282-5
5	3741	97.7	739	9	US-09-912-157-8
6	3741	97.7	739	15	US-10-717-282-8
7	3731	97.4	739	16	US-10-842-006-2
8	3731	97.4	739	16	US-10-608-449-2
9	3729	97.4	739	16	US-10-842-006-4
10	3725	97.3	738	9	US-09-809-567-2
11	3725	97.3	738	14	US-10-216-156-2

12	3725	97.3	738	15	US-10-616-788-2	Sequence 2, Appli
13	3708	96.8	728	15	US-10-104-047-3399	Sequence 3399, Ap
14	3703	96.7	728	9	US-09-874-503-18	Sequence 18, Appl
15	3703	96.7	728	10	US-09-816-744-18	Sequence 18, Appl
16	3703	96.7	728	10	US-09-747-259-18	Sequence 18, Appl
17	3703	96.7	728	10	US-09-908-827-18	Sequence 18, Appl
18	3703	96.7	728	13	US-10-000-157-18	Sequence 18, Appl
19	3703	96.7	728	14	US-10-410-927-18	Sequence 18, Appl
20	3703	96.7	728	14	US-10-410-374-18	Sequence 18, Appl
21	3703	96.7	728	14	US-10-410-552-18	Sequence 18, Appl
22	3703	96.7	728	15	US-10-458-442-18	Sequence 18, Appl
23	3703	96.7	728	15	US-10-408-385-18	Sequence 18, Appl
24	3657.5	95.5	738	10	US-09-863-818A-10	Sequence 10, Appl
25	3657.5	95.5	738	16	US-10-749-144-10	Sequence 10, Appl
26	3657.5	95.5	738	17	US-10-924-667-10	Sequence 10, Appl
27	3208	83.8	739	9	US-09-912-157-12	Sequence 12, Appl
28	3208	83.8	739	15	US-10-717-282-12	Sequence 12, Appl
29	3176	82.9	595	17	US-10-477-714-16	Sequence 16, Appl
30	3170	82.8	595	16	US-10-608-449-4	Sequence 4, Appli
31	2515.5	65.7	554	15	US-10-343-348-16	Sequence 16, Appl
32	1334	34.8	296	15	US-10-616-788-19	Sequence 19, Appl
33	312	8.1	810	9	US-09-809-567-3	Sequence 3, Appli
34	312	8.1	810	14	US-10-216-156-3	Sequence 3, Appli
35	312	8.1	810	15	US-10-616-788-3	Sequence 3, Appli
36	312	8.1	866	9	US-09-778-971-9	Sequence 9, Appli
37	312	8.1	866	13	US-10-033-522-1	Sequence 1, Appli
38	312	8.1	866	14	US-10-207-655-107	Sequence 107, App
39	312	8.1	866	16	US-10-742-161-10	Sequence 10, Appl
40	312	8.1	866	16	US-10-742-372-10	Sequence 10, Appl
41	312	8.1	866	16	US-10-646-308-4	Sequence 4, Appli
42	312	8.1	866	17	US-10-318-084-1	Sequence 1, Appli
43	306	8.0	864	16	US-10-742-161-2	Sequence 2, Appli
44	306	8.0	864	16	US-10-742-372-2	Sequence 2, Appli
45	232.5	6.1	207	10	US-09-863-818A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-912-157-2
; Sequence 2, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912.157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-2

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Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	718;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	36	ADTCGWRKAAARPRCLVANEGVGPASRNSGLYNTFKYDNC	36	ADTCGWRKAAARPRCLVANEGVGPASRNSGLYNTFKYDNC	36	ADTCGWRKAAARPRCLVANEGVGPASRNSGLYNTFKYDNC	36
Qy	61	TISQVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQLNSFFK	61	TISQVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQLNSFFK	61	TISQVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQLNSFFK	61
Db	96	TISQVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQLNSFFK	96	TISQVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQLNSFFK	96	TISQVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQLNSFFK	96
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Db							

Db 156 RTGMESQPLNMKFETDVFVKVPPPSIKNESNYHPPFTRACDILLQPDNLACKPFWK 215
Qy 181 PRNLNISQHSQDMQVSPDHAPHNFGFRFFYLHYKLKHGPPKRTCKQEQTTETTSCLLQ 240
Db 216 PRNLNISQHSQDMQVSPDHAPHNFGFRFFYLHYKLKHGPPKRTCKQEQTTETTSCLLQ 275
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPTRAVALITVPLVVISAFATLFTVMC 300
Db 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPTRAVALITVPLVVISAFATLFTVMC 335
Qy 301 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFL 360
Db 336 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFL 395
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Db 396 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 455
Qy 421 RSGKGELFLVAVSAIAEKLROAKOSSAALSKEFIAYVFDYSCGDVPGILDLSKTYRLM 480
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RESULT 2

US-10-717-282-2

; Sequence 2, Application US/10717282

; Publication No. US20040077052A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/10/717,282

; CURRENT FILING DATE: 2003-11-19

; PRIOR APPLICATION NUMBER: US/09/912,157

; PRIOR FILING DATE: 2001-07-24

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-717-282-2

Query Match 100.0%; Score 3829; DB 15; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 36 ADTCGRMKAAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIADAQNI 95
Qy 61 TISQYACHDQAVATILMSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKQNLSSFK 120
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Qy 121 RTGMESQPLNMKFETDVFVKVPPPSIKNESNYHPPFTRACDILLQPDNLACKPFWK 180
Db 156 RTGMESQPLNMKFETDVFVKVPPPSIKNESNYHPPFTRACDILLQPDNLACKPFWK 215
Qy 181 PRNLNISQHSQDMQVSPDHAPHNFGFRFFYLHYKLKHGPPKRTCKQEQTTETTSCLLQ 240
Db 216 PRNLNISQHSQDMQVSPDHAPHNFGFRFFYLHYKLKHGPPKRTCKQEQTTETTSCLLQ 275
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPTRAVALITVPLVVISAFATLFTVMC 300
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Db 336 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFL 395
Qy 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 420
Db 396 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 455
Qy 421 RSGKGELFLVAVSAIAEKLROAKOSSAALSKEFIAYVFDYSCGDVPGILDLSKTYRLM 480
Db 456 RSGKGELFLVAVSAIAEKLROAKOSSAALSKEFIAYVFDYSCGDVPGILDLSKTYRLM 515
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RESULT 3

US-09-912-157-5

; Sequence 5, Application US/09912157

; Patent No. US20020165348A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-157-5

Query Match 99.7%; Score 3819; DB 9; Length 753;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 96 TISQYACHDQAVATILMSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKQNLSSFK 155

QY 121 RTGMSOPFLNMKFETDYFKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 180
DB 156 RTGMSOPFLNMKFETDYFKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 215
QY 181 PRNLNISOHSDMQVSPDHAPHNFGPRFFYLHYKLKHEGPPFKRTCKOBTETTSCLLQ 240
DB 216 PRNLNISOHSDMQVSPDHAPHNFGPRFFYLHYKLKHEGPPFKRTCKOBTETTSCLLQ 275
QY 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
DB 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
QY 301 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 360
DB 336 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 395
QY 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 420
DB 396 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 455
QY 421 RGSKGELFLVAVSAIAEKLROAKOSSAALSKEIANYFYDYSCGDPVGIILDLSTKYRLM 480
DB 456 RGSKGELFLVAVSAIAEKLROAKOSSAALSKEIANYFYDYSCGDPVGIILDLSTKYRLM 515
QY 481 DNLQOLCSHLHSRDHGLQEPQOHTROGSRNNYFRSKSGRSLYVAICNNHQFIDBEPDWE 540
DB 516 DNLQOLCSHLHSRDHGLQEPQOHTROGSRNNYFRSKSGRSLYVAICNNHQFIDBEPDWE 575
QY 541 KQFVFPFPPPLRYREPVLKFDGLVLDVNDVCMKPGPESDFCLKVEAAVLGATGADSOHE 600
DB 576 KQFVFPFPPPLRYREPVLKFDGLVLDVNDVCMKPGPESDFCLKVEAAVLGATGADSOHE 635
QY 601 SOHGLDQDGEARPALDGSAAALQPLLTHTVKAGSPDMPDRSGIYDSSVSPSELSPLMEG 660
DB 636 SOHGLDQDGEARPALDGSAAALQPLLTHTVKAGSPDMPDRSGIYDSSVSPSELSPLMEG 695
QY 661 LSTDQTTSSLTESVSSSSGLGEEPPALPKLLSSGCKADLCRSYTDLHVAAPL 718
DB 696 LSTDQTTSSLTESVSSSSGLGEEPPALPKLLSSGCKADLCRSYTDLHVAAPL 753

RESULT 4

US-10-717-282-5
; Sequence 5, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-282-5

Query Match 99.7%; Score 3819; DB 15; Length 753;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGVKHVIADAQNI 60
DB 36 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGVKHVIADAQNI 95
QY 61 TISQYACHDQVAVTILWSPGALGIEFLKGRFVILLEELKSEGRQCOOLILKDPKOLNSFK 120

DB 96 TISQYACHDQVAVTILWSPGALGIEFLKGRFVILLEELKSEGRQCOOLILKDPKOLNSFK 155
QY 121 RTGMSOPFLNMKFETDYFKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 180
DB 156 RTGMSOPFLNMKFETDYFKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 215
QY 181 PRNLNISOHSDMQVSPDHAPHNFGPRFFYLHYKLKHEGPPFKRTCKOBTETTSCLLQ 240
DB 216 PRNLNISOHSDMQVSPDHAPHNFGPRFFYLHYKLKHEGPPFKRTCKOBTETTSCLLQ 275
QY 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
DB 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
QY 301 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 360
DB 336 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 395
QY 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 420
DB 396 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 455
QY 421 RGSKGELFLVAVSAIAEKLROAKOSSAALSKEIANYFYDYSCGDPVGIILDLSTKYRLM 480
DB 456 RGSKGELFLVAVSAIAEKLROAKOSSAALSKEIANYFYDYSCGDPVGIILDLSTKYRLM 515
QY 481 DNLQOLCSHLHSRDHGLQEPQOHTROGSRNNYFRSKSGRSLYVAICNNHQFIDBEPDWE 540
DB 516 DNLQOLCSHLHSRDHGLQEPQOHTROGSRNNYFRSKSGRSLYVAICNNHQFIDBEPDWE 575
QY 541 KQFVFPFPPPLRYREPVLKFDGLVLDVNDVCMKPGPESDFCLKVEAAVLGATGADSOHE 600
DB 576 KQFVFPFPPPLRYREPVLKFDGLVLDVNDVCMKPGPESDFCLKVEAAVLGATGADSOHE 635
QY 601 SOHGLDQDGEARPALDGSAAALQPLLTHTVKAGSPDMPDRSGIYDSSVSPSELSPLMEG 660
DB 636 SOHGLDQDGEARPALDGSAAALQPLLTHTVKAGSPDMPDRSGIYDSSVSPSELSPLMEG 695
QY 661 LSTDQTTSSLTESVSSSSGLGEEPPALPKLLSSGCKADLCRSYTDLHVAAPL 718
DB 696 LSTDQTTSSLTESVSSSSGLGEEPPALPKLLSSGCKADLCRSYTDLHVAAPL 753

RESULT 5

US-09-912-157-8
; Sequence 8, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-8

Query Match 97.7%; Score 3741; DB 9; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 704; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
QY 1 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGVKHVIADAQNI 60
DB 36 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGVKHVIADAQNI 81
QY 61 TISQYACHDQVAVTILWSPGALGIEFLKGRFVILLEELKSEGRQCOOLILKDPKOLNSFK 120


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Db      82  TISQACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCCQLILKDPKQLNSSFK 141
Qy      121  RTGMSQPFLLNMKFETDYFVKVVPFPIKNESNYHPFFFRTRACDILLQDNLACKPFWK 180
Db      142  RTGMSQPFLLNMKFETDYFVKVVPFPIKNESNYHPFFFRTRACDILLQDNLACKPFWK 201
Qy      181  PRNLNISOHSGDMQVSDHAPHNFGPRFFVLYHLKHGEPFKRTCKQBOTTTTSCLLQ 240
Db      202  PRNLNISOHSGDMQVSDHAPHNFGPRFFVLYHLKHGEPFKRTCKQBOTTTTSCLLQ 261
Qy      241  NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db      262  NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy      301  RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFYL 360
Db      322  RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFYL 381
Qy      361  QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 420
Db      382  QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 441
Qy      421  RSGKGELFLVAVSAIAEKLRAQAKQSSSAALSKEFIAVYFDYSCGDVPGILDSTKYRLM 480
Db      442  RSGKGELFLVAVSAIAEKLRAQAKQSSSAALSKEFIAVYFDYSCGDVPGILDSTKYRLM 501
Qy      481  DNLPLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSLYVAICNMHOFIDEEPWF 540
Db      502  DNLPLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSLYVAICNMHOFIDEEPWF 561
Qy      541  KQFVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db      562  KQFVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy      601  SQHGGLDQDGEARALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 660
Db      622  SQHGGLDQDGEARALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 681
Qy      661  LSTDQTETSSLTSSVSSSGLGEEPPALPKLLSSGSKADLCGRSYTDELHVAAPL 718
Db      682  LSTDQTETSSLTSSVSSSGLGEEPPALPKLLSSGSKADLCGRSYTDELHVAAPL 739
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RESULT 6

US-10-717-282-8

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; Sequence 8, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-282-8
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Query Match          97.7%; Score 3741; DB 15; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 704; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
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Qy      1  ADTCGWRMKAARPRLCVANEVGPASRNSGLYNTFKYDNCCTTYLNPVGHVIAQAQNI 60
Db      36  ADTCGWR-----GVGPASRNSGLYNTFKYDNCCTTYLNPVGHVIAQAQNI 81
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Qy      61  TISQACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCCQLILKDPKQLNSSFK 120
Db      82  TISQACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCCQLILKDPKQLNSSFK 141
Qy      121  RTGMSQPFLLNMKFETDYFVKVVPFPIKNESNYHPFFFRTRACDILLQDNLACKPFWK 180
Db      142  RTGMSQPFLLNMKFETDYFVKVVPFPIKNESNYHPFFFRTRACDILLQDNLACKPFWK 201
Qy      181  PRNLNISOHSGDMQVSDHAPHNFGPRFFVLYHLKHGEPFKRTCKQBOTTTTSCLLQ 240
Db      202  PRNLNISOHSGDMQVSDHAPHNFGPRFFVLYHLKHGEPFKRTCKQBOTTTTSCLLQ 261
Qy      241  NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db      262  NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy      301  RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFYL 360
Db      322  RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFYL 381
Qy      361  QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 420
Db      382  QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 441
Qy      421  RSGKGELFLVAVSAIAEKLRAQAKQSSSAALSKEFIAVYFDYSCGDVPGILDSTKYRLM 480
Db      442  RSGKGELFLVAVSAIAEKLRAQAKQSSSAALSKEFIAVYFDYSCGDVPGILDSTKYRLM 501
Qy      481  DNLPLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSLYVAICNMHOFIDEEPWF 540
Db      502  DNLPLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSLYVAICNMHOFIDEEPWF 561
Qy      541  KQFVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db      562  KQFVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy      601  SQHGGLDQDGEARALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 660
Db      622  SQHGGLDQDGEARALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 681
Qy      661  LSTDQTETSSLTSSVSSSGLGEEPPALPKLLSSGSKADLCGRSYTDELHVAAPL 718
Db      682  LSTDQTETSSLTSSVSSSGLGEEPPALPKLLSSGSKADLCGRSYTDELHVAAPL 739
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RESULT 7

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US-10-842-006-2
; Sequence 2, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: MPI03-071PIRM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-006-2
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Query Match          97.4%; Score 3731; DB 16; Length 739;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 702; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
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```
Qy      1  ADTCGWRMKAARPRLCVANEVGPASRNSGLYNTFKYDNCCTTYLNPVGHVIAQAQNI 60
Db      36  ADTCGWR-----GVGPASRNSGLYNTFKYDNCCTTYLNPVGHVIAQAQNI 81
```

Qy 61 TISQACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRCQCOQLILKDPKOLNSSFK 120
Db 82 TISQACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRCQCOQLILKDPKOLNSSFK 141
Qy 121 RTGMSQPFLLNMKFETDYFVKVVPFPIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 180
Db 142 RTGMSQPFLLNMKFETDYFVKVVPFPIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 201
Qy 181 PRNLISQHSQDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRTCKOQOTETTSCILQ 240
Db 202 PRNLISQHSQDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRTCKOQOTETTSCILQ 261
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 262 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy 301 RKQOENIYSHLDEESSESYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCFAYFL 360
Db 322 RKQOENIYSHLDEESSESYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCFAYFL 381
Qy 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 420
Db 382 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 441
Qy 421 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHKG 480
Db 442 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHKG 501
Qy 481 DNLQCLSHLSRDHGLQEPQOHTROGSRNRYFRSKSGRSIYVAICNMHQFIDEEPWF 540
Db 502 DNLQCLSHLSRDHGLQEPQOHTROGSRNRYFRSKSGRSIYVAICNMHQFIDEEPWF 561
Qy 541 KQFVFPHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db 562 KQFVFPHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy 601 SOHGLDQDGEARALDGSAAALQPLHTVTRKAGSPDMRDSGIYDSSVPSSLSPLMEG 660
Db 622 SOHGLDQDGEARALDGSAAALQPLHTVTRKAGSPDMRDSGIYDSSVPSSLSPLMEG 681
Qy 661 LSTQOTETSSITSVSSSSGLGEEPPALPSKLLSSGSKADLCGRSYTDELHAVA 718
Db 682 LSTQOTETSSITSVSSSSGLGEEPPALPSKLLSSGSKADLCGRSYTDELHAVA 739

RESULT 8
US-10-608-449-2
; Sequence 2, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Tsinghua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: I2003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-608-449-2

Query Match 97.4%; Score 3731; DB 16; Length 739;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 702; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
Qy 1 ADTCGRWKAARPLCLVANEGVGPASRNSGLYNTTFKYDNCCTTYLNPVGKHVIAQA 60
Db 36 ADTCGRW-----GVGPASRNSGLYNTTFKYDNCCTTYLNPVGKHVIAQA 81
Qy 61 TISQACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRCQCOQLILKDPKOLNSSFK 120

Db 82 TISQACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRCQCOQLILKDPKOLNSSFK 141
Qy 121 RTGMSQPFLLNMKFETDYFVKVVPFPIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 180
Db 142 RTGMSQPFLLNMKFETDYFVKVVPFPIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 201
Qy 181 PRNLISQHSQDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRTCKOQOTETTSCILQ 240
Db 202 PRNLISQHSQDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRTCKOQOTETTSCILQ 261
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 262 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy 301 RKQOENIYSHLDEESSESYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCFAYFL 360
Db 322 RKQOENIYSHLDEESSESYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCFAYFL 381
Qy 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 420
Db 382 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 441
Qy 421 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHKG 480
Db 442 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHKG 501
Qy 481 DNLQCLSHLSRDHGLQEPQOHTROGSRNRYFRSKSGRSIYVAICNMHQFIDEEPWF 540
Db 502 DNLQCLSHLSRDHGLQEPQOHTROGSRNRYFRSKSGRSIYVAICNMHQFIDEEPWF 561
Qy 541 KQFVFPHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db 562 KQFVFPHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy 601 SOHGLDQDGEARALDGSAAALQPLHTVTRKAGSPDMRDSGIYDSSVPSSLSPLMEG 660
Db 622 SOHGLDQDGEARALDGSAAALQPLHTVTRKAGSPDMRDSGIYDSSVPSSLSPLMEG 681
Qy 661 LSTQOTETSSITSVSSSSGLGEEPPALPSKLLSSGSKADLCGRSYTDELHAVA 718
Db 682 LSTQOTETSSITSVSSSSGLGEEPPALPSKLLSSGSKADLCGRSYTDELHAVA 739

RESULT 9
US-10-842-006-4
; Sequence 4, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: MP103-071P1RM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-006-4

Query Match 97.4%; Score 3729; DB 16; Length 739;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 701; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
Qy 2 DTCCWRKMAARPLCLVANEGVGPASRNSGLYNTTFKYDNCCTTYLNPVGKHVIAQA 61
Db 37 DTCCWR-----GVGPASRNSGLYNTTFKYDNCCTTYLNPVGKHVIAQA 82

Qy 62 ISOYACHDOVAVTILWSPGALGIEFLKGRFVRVILBELKSEGRQCOQLILKDPKQLNSSFKR 121
Db 83 ISOYACHDOVAVTILWSPGALGIEFLKGRFVRVILBELKSEGRQCOQLILKDPKQLNSSFKR 142
Qy 122 TGMESQPFLLNMKFETDYFVKVVPFSPISKNESNYHPPFRTRACDILLQPNLACKPFWKP 181
Db 143 TGMESQPFLLNMKFETDYFVKVVPFSPISKNESNYHPPFRTRACDILLQPNLACKPFWKP 202
Qy 182 RNLNISQHGSDMOVSFDHAPHNFGFRFFYLHYKLKHEGPPFRKTKCKOEOQTETTSCLLON 241
Db 203 RNLNISQHGSDMOVSFDHAPHNFGFRFFYLHYKLKHEGPPFRKTKCKOEOQTETTSCLLON 262
Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 301
Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322
Qy 302 KQOENIYSHLDESSSSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
Db 323 KQOENIYSHLDESSSSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 382
Qy 362 DFCCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
Db 383 DFCCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
Qy 422 GSGKGELFLVAVSAIAEKLROAKOSSAALSCKFIATVDFYSCGDVPGIILDLSTKYRLMD 481
Db 443 GSGKGELFLVAVSAIAEKLROAKOSSAALSCKFIATVDFYSCGDVPGIILDLSTKYRLMD 502
Qy 482 NLPOLCSHLHRDGLQEPGQHTROGSRNNYFRSKGSRSLYVAICNNHQFIDEEPWFKEK 541
Db 503 NLPOLCSHLHRDGLQEPGQHTROGSRNNYFRSKGSRSLYVAICNNHQFIDEEPWFKEK 562
Qy 542 QFVFPHPPLRYRREPVLKFDGSLVLDVNMCKPGPESDFCLKVEAAVLGATGPADSQSHES 601
Db 563 QFVFPHPPLRYRREPVLKFDGSLVLDVNMCKPGPESDFCLKVEAPVLGATGPADSQSHES 622
Qy 602 QHGGLDODGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGL 661
Db 623 QHGGLDODGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGL 682
Qy 662 STDQTTSSLTSSVSSSGLGEEBPPALPSKLLSSGCKADLGCRTYDELHVAAPL 718
Db 683 STDQTTSSLTSSVSSSGLGEEBPPALPSKLLSSGCKADLGCRTYDELHVAAPL 739

RESULT 10
US-09-567-2
; Sequence 2, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/09/809,567
; CURRENT FILING DATE: 2001-03-15
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-567-2

Query Match 97.3%; Score 3725; DB 9; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 2 DTCGWRKAAARPRLCVANEVGVGSPASRNSGLYNTTFKYDNCCTTYLNPVGVKHVIADAQNIT 61
|||||

Db 37 DTCGWR-----GVGPASRNSGLYNTTFKYDNCCTTYLNPVGVKHVIADAQNIT 82
Qy 62 ISOYACHDOVAVTILWSPGALGIEFLKGRFVRVILBELKSEGRQCOQLILKDPKQLNSSFKR 121
Db 83 ISOYACHDOVAVTILWSPGALGIEFLKGRFVRVILBELKSEGRQCOQLILKDPKQLNSSFKR 142
Qy 122 TGMESQPFLLNMKFETDYFVKVVPFSPISKNESNYHPPFRTRACDILLQPNLACKPFWKP 181
Db 143 TGMESQPFLLNMKFETDYFVKVVPFSPISKNESNYHPPFRTRACDILLQPNLACKPFWKP 202
Qy 182 RNLNISQHGSDMOVSFDHAPHNFGFRFFYLHYKLKHEGPPFRKTKCKOEOQTETTSCLLON 241
Db 203 RNLNISQHGSDMOVSFDHAPHNFGFRFFYLHYKLKHEGPPFRKTKCKOEOQTETTSCLLON 262
Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 301
Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322
Qy 302 KQOENIYSHLDESSSSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
Db 323 KQOENIYSHLDESSSSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 382
Qy 362 DFCCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
Db 383 DFCCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
Qy 422 GSGKGELFLVAVSAIAEKLROAKOSSAALSCKFIATVDFYSCGDVPGIILDLSTKYRLMD 481
Db 443 GSGKGELFLVAVSAIAEKLROAKOSSAALSCKFIATVDFYSCGDVPGIILDLSTKYRLMD 502
Qy 482 NLPOLCSHLHRDGLQEPGQHTROGSRNNYFRSKGSRSLYVAICNNHQFIDEEPWFKEK 541
Db 503 NLPOLCSHLHRDGLQEPGQHTROGSRNNYFRSKGSRSLYVAICNNHQFIDEEPWFKEK 562
Qy 542 QFVFPHPPLRYRREPVLKFDGSLVLDVNMCKPGPESDFCLKVEAAVLGATGPADSQSHES 601
Db 563 QFVFPHPPLRYRREPVLKFDGSLVLDVNMCKPGPESDFCLKVEAPVLGATGPADSQSHES 622
Qy 602 QHGGLDODGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGL 661
Db 623 QHGGLDODGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGL 682
Qy 662 STDQTTSSLTSSVSSSGLGEEBPPALPSKLLSSGCKADLGCRTYDELHVAAP 717
Db 683 STDQTTSSLTSSVSSSGLGEEBPPALPSKLLSSGCKADLGCRTYDELHVAAP 738

RESULT 11
US-10-216-156-2
; Sequence 2, Application US/10216156
; Publication No. US2003009980A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/10/216,156
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US/09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-156-2

Query Match 97.3%; Score 3725; DB 14; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;

Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 2 DTCGRMKAAARPRLCVANEGVGPASRNSGLYNTFFKYDNCCTTVLPNPGKHVIADAQNIT 61
Db |||||
Qy 37 DTCGWR-----GVGPASRNSGLYNTFFKYDNCCTTVLPNPGKHVIADAQNIT 82
Db |||||

Qy 62 ISOYACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRQCQOLILKDPKQLNSSFKR 121
Db |||||

Qy 83 ISOYACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRQCQOLILKDPKQLNSSFKR 142
Db |||||

Qy 122 TGMESQPLNMKFTDYFVKVVPFPPSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWKP 181
Db |||||

Qy 143 TGMESQPLNMKFTDYFVKVVPFPPSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWKP 202
Db |||||

Qy 182 RNLNISQHSQDMQVSFDHAPNFGFRFYLYHKLKHEGPPFRKTKCKOEQTETTSCLLON 241
Db |||||

Qy 203 RNLNISQHSQDMQVSFDHAPNFGFRFYLYHKLKHEGPPFRKTKCKOEQTETTSCLLON 262
Db |||||

Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 301
Db |||||

Qy 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 322
Db |||||

Qy 302 KQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYPLQ 361
Db |||||

Qy 323 KQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYPLQ 382
Db |||||

Qy 362 DFCCEVALDWDPSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGR 421
Db |||||

Qy 383 DFCCEVALDWDPSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGR 442
Db |||||

Qy 422 GSGKGEFLVAVSAIAEKLROAKOSSAALSKEFTAVFYDSCGDPVPGILDSTKYRLMD 481
Db |||||

Qy 443 GSGKGEFLVAVSAIAEKLROAKOSSAALSKEFTAVFYDSCGDPVPGILDSTKYRLMD 502
Db |||||

Qy 482 NLPQLCSHLHRDGLQBPQGHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDPFEK 541
Db |||||

Qy 503 NLPQLCSHLHRDGLQBPQGHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDPFEK 562
Db |||||

Qy 542 QFVFPHPPLRYREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHES 601
Db |||||

Qy 563 QFVFPHPPLRYREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHES 622
Db |||||

Qy 602 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMBGL 661
Db |||||

Qy 623 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMBGL 682
Db |||||

Qy 662 STDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDELHAVAP 717
Db |||||

Qy 683 STDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDELHAVAP 738
Db |||||

RESULT 12

US-10-616-788-2

; Sequence 2, Application US/10616788

; Publication No. US20040048338A1

; GENERAL INFORMATION:

; APPLICANT: Jing, Shuqian

; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof

; FILE REFERENCE: 01017/39525

; CURRENT APPLICATION NUMBER: US/10/616,788

; CURRENT FILING DATE: 2003-07-10

; PRIOR APPLICATION NUMBER: 09/809,567

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 09/724,460

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 60/189,816

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 2

; LENGTH: 738

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-616-788-2

Query Match 97.3%; Score 3725; DB 15; Length 738;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 2 DTCGRMKAAARPRLCVANEGVGPASRNSGLYNTFFKYDNCCTTVLPNPGKHVIADAQNIT 61
Db |||||

Qy 37 DTCGWR-----GVGPASRNSGLYNTFFKYDNCCTTVLPNPGKHVIADAQNIT 82
Db |||||

Qy 62 ISOYACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRQCQOLILKDPKQLNSSFKR 121
Db |||||

Qy 83 ISOYACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRQCQOLILKDPKQLNSSFKR 142
Db |||||

Qy 122 TGMESQPLNMKFTDYFVKVVPFPPSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWKP 181
Db |||||

Qy 143 TGMESQPLNMKFTDYFVKVVPFPPSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWKP 202
Db |||||

Qy 182 RNLNISQHSQDMQVSFDHAPNFGFRFYLYHKLKHEGPPFRKTKCKOEQTETTSCLLON 241
Db |||||

Qy 203 RNLNISQHSQDMQVSFDHAPNFGFRFYLYHKLKHEGPPFRKTKCKOEQTETTSCLLON 262
Db |||||

Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 301
Db |||||

Qy 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 322
Db |||||

Qy 302 KQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYPLQ 361
Db |||||

Qy 323 KQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYPLQ 382
Db |||||

Qy 362 DFCCEVALDWDPSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGR 421
Db |||||

Qy 383 DFCCEVALDWDPSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGR 442
Db |||||

Qy 422 GSGKGEFLVAVSAIAEKLROAKOSSAALSKEFTAVFYDSCGDPVPGILDSTKYRLMD 481
Db |||||

Qy 443 GSGKGEFLVAVSAIAEKLROAKOSSAALSKEFTAVFYDSCGDPVPGILDSTKYRLMD 502
Db |||||

Qy 482 NLPQLCSHLHRDGLQBPQGHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDPFEK 541
Db |||||

Qy 503 NLPQLCSHLHRDGLQBPQGHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDPFEK 562
Db |||||

Qy 542 QFVFPHPPLRYREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHES 601
Db |||||

Qy 563 QFVFPHPPLRYREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHES 622
Db |||||

Qy 602 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMBGL 661
Db |||||

Qy 623 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMBGL 682
Db |||||

Qy 662 STDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDELHAVAP 717
Db |||||

Qy 683 STDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDELHAVAP 738
Db |||||

RESULT 13

US-10-104-047-3399

; Sequence 3399, Application US/10104047

; Publication No. US20030236392A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. US20030236392A1el full length cDNA

; FILE REFERENCE: H1-A0105

; CURRENT APPLICATION NUMBER: US/10/104,047

; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER:

; PRIOR FILING DATE:

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 3399

; LENGTH: 728

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-104-047-3399

Query Match 96.8%; Score 3708; DB 15; Length 728;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 21 EGVGPASRNSGLNITFKYDNCCTTYLNPVGKHVADAGNITISQYACHDQVAVTILMSPG 80
Db :|||||
Qy 31 QGVGPASRNSGLNITFKYDNCCTTYLNPVGKHVADAGNITISQYACHDQVAVTILMSPG 90
Db :|||||
Qy 81 ALGIEFLKGRFVILLEELKSEGRQCOQLILDKPKQLNSFKRTGMESQFFLNKMFETDYFV 140
Db :|||||
Qy 91 ALGIEFLKGRFVILLEELKSEGRQCOQLILDKPKQLNSFKRTGMESQFFLNKMFETDYFV 150
Db :|||||
Qy 141 KVPFPPIKESNTHPFFRTRACDILLQPNLACKPFWKPRNINI SHGSDMQVSPDHA 200
Db :|||||
Qy 151 KVPFPPIKESNTHPFFRTRACDILLQPNLACKPFWKPRNINI SHGSDMQVSPDHA 210
Db :|||||
Qy 201 PHNFGFRFFYLHYKLKHEGPFKRTCKOEQTETTSCLLQNVSPGDYIIELVDDTNTTRK 260
Db :|||||
Qy 211 PHNFGFRFFYLHYKLKHEGPFKRTCKOEQTETTSCLLQNVSPGDYIIELVDDTNTTRK 270
Db :|||||
Qy 261 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESESS 320
Db :|||||
Qy 271 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESESS 330
Db :|||||
Qy 321 TYTAALPRERLRPRPKVFLCYSSKQGNHNVVQCFAFYFLQDFCGCEVALDLNEDFSLCR 380
Db :|||||
Qy 331 TYTAALPRERLRPRPKVFLCYSSKQGNHNVVQCFAFYFLQDFCGCEVALDLNEDFSLCR 390
Db :|||||
Qy 381 EGQREWIQKHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGLFLVAVSAIAEKL 440
Db :|||||
Qy 391 EGQREWIQKHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGLFLVAVSAIAEKL 450
Db :|||||
Qy 441 RQAKQSSAALSKEFIAYVDFYSCEDVPGILDLSTKYRLMDNLPLQCLSHLSRDHGLQEP 500
Db :|||||
Qy 451 RQAKQSSAALSKEFIAYVDFYSCEDVPGILDLSTKYRLMDNLPLQCLSHLSRDHGLQEP 510
Db :|||||
Qy 501 GQHTQSSRRNYFRSKGRSLYVAICNMHQIDEPDMWFEKFVFPFPPPLRYREPVLK 560
Db :|||||
Qy 511 GQHTQSSRRNYFRSKGRSLYVAICNMHQIDEPDMWFEKFVFPFPPPLRYREPVLK 570
Db :|||||
Qy 561 FDSGLVLNDVCKPGPSDFCLKVEAAVLGATGADSOHESQHGGLQDGEARPALDQSA 620
Db :|||||
Qy 571 FDSGLVLNDVCKPGPSDFCLKVEAAVLGATGADSOHESQHGGLQDGEARPALDQSA 630
Db :|||||
Qy 621 ALQPLLHTVKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDTQTETSSLITESVSSSG 680
Db :|||||
Qy 631 ALQPLLHTVKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDTQTETSSLITESVSSSG 690
Db :|||||
Qy 681 LGEEPPALPSKLLSSGSKADLCGRSYTDLHVAAPL 718
Db :|||||
Qy 691 LGEEPPALPSKLLSSGSKADLCGRSYTDLHVAAPL 728
Db :|||||

RESULT 14

US-09-874-503-18
Sequence 18, Application US/09874503
Patent No. US20020177188A1

GENERAL INFORMATION:

APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hymowitz, Sarah G.
APPLICANT: Tumas, Daniel
APPLICANT: Starovasnik, Melissa A.
APPLICANT: VanLookeren, Menno

APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P3 (US)
CURRENT APPLICATION NUMBER: US/09/874, 503
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/253, 646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/244, 072
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/242, 837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/175, 481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 60/191, 007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/213, 807
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/172, 096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/138, 387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: US 60/134, 287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/131, 022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: US 60/130, 232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/113, 621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/085, 579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 09/854, 208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854, 280
PRIOR FILING DATE: 2001-05-20
PRIOR APPLICATION NUMBER: US 09/816, 744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/747, 259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/644, 848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/380, 142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/380, 138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/311, 832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US PCT/US99/31274
PRIOR FILING DATE: 1999-12-30

;; PRIOR APPLICATION NUMBER: US PCT/US99/10733
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 18
;; LENGTH: 728
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-874-503-18

Query Match 96.7%; Score 3703; DB 9; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

Qy 7 RMKAAAPRLCVANE-GVGPASRNSGLYNTIFKVDNCTTYLNPVKGKVIADAQNITISQY 65
Db 3 RASAGVPALFVSGEQGVGPASRNSGLYNTIFKVDNCTTYLNPVKGKVIADAQNITISQY 62

Qy 66 ACHDOQAVTILWSPGALGIEFLKGRVILELSEKSGRQCQOLILKDPKQLNSSFRTGME 125
Db 63 ACHDOQAVTILWSPGALGIEFLKGRVILELSEKSGRQCQOLILKDPKQLNSSFRTGME 122

Qy 126 SQPLFNKMFETDYFKVVPFPIKESNYHFFRTRACDILLQPDNLACKPFWKPRNLN 185
Db 123 SQPLFNKMFETDYFKVVPFPIKESNYHFFRTRACDILLQPDNLACKPFWKPRNLN 182

Qy 186 ISQ-----HGSDMQVDFDHAPHNFGFRFFLHYKLHKGEPFKKTCQEQTT 232
Db 183 ISQHGSDMQVDFDHAPHNFGFRFFLHYKLHKGEPFKKTCQEQTT 242

Qy 233 ETTSCLLQNVSPGDIYIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
Db 243 EMTSCLLQNVSPGDIYIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302

Qy 293 ATLFTVMCRKQKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHNV 352
Db 303 ATLFTVMCRKQKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHNV 362

Qy 353 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKHESQFIIVVCSKGMKVFVDKK 412
Db 363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKHESQFIIVVCSKGMKVFVDKK 422

Qy 413 NYKHGGGRGSGKGEFLVAVSAEKLRAQKSSAALSKEFIAYFYDYSCEGDVPGILD 472
Db 423 NYKHGGGRGSGKGEFLVAVSAEKLRAQKSSAALSKEFIAYFYDYSCEGDVPGILD 482

Qy 473 LSTKYRLMDNLPQLCSHLHSDHGLQEPQHTROGSRNRYFRSKSGRSLYVAICNMHQFI 532
Db 483 LSTKYRLMDNLPQLCSHLHSDHGLQEPQHTROGSRNRYFRSKSGRSLYVAICNMHQFI 542

Qy 533 DEEDPWFEKQVFPFHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 592
Db 543 DEEDPWFEKQVFPFHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 602

Qy 593 GPADSQHSQHGGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMPRDSGIYDSSVPSSE 652
Db 603 GPADSQHSQHGGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMPRDSGIYDSSVPSSE 662

Qy 653 LSLPLMEGLSTDQTTSTISVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSYTDEL 712
Db 663 LSLPLMEGLSTDQTTSTISVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSYTDEL 722

Qy 713 HAVAPL 718
Db 723 HAVAPL 728

RESULT 15
US-09-816-744-18
; Sequence 18, Application US/09816744
; Publication No. US20030003546A1
; GENERAL INFORMATION:

;; APPLICANT: Chen, Jian
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Li, Hanzhong
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Tumas, Daniel
;; APPLICANT: VanLookeren, Menno
;; APPLICANT: Vandlen, Richard
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William
;; APPLICANT: Yansura, Daniel
;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;; FILE REFERENCE: P1381R1C1P2(US)
;; CURRENT APPLICATION NUMBER: US/09/816,744
;; CURRENT FILING DATE: 2001-03-22
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 18
;; LENGTH: 728
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-816-744-18

Query Match 96.7%; Score 3703; DB 10; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

Qy 7 RMKAAAPRLCVANE-GVGPASRNSGLYNTIFKVDNCTTYLNPVKGKVIADAQNITISQY 65
Db 3 RASAGVPALFVSGEQGVGPASRNSGLYNTIFKVDNCTTYLNPVKGKVIADAQNITISQY 62

Qy 66 ACHDOQAVTILWSPGALGIEFLKGRVILELSEKSGRQCQOLILKDPKQLNSSFRTGME 125
Db 63 ACHDOQAVTILWSPGALGIEFLKGRVILELSEKSGRQCQOLILKDPKQLNSSFRTGME 122

Qy 126 SQPLFNKMFETDYFKVVPFPIKESNYHFFRTRACDILLQPDNLACKPFWKPRNLN 185
Db 123 SQPLFNKMFETDYFKVVPFPIKESNYHFFRTRACDILLQPDNLACKPFWKPRNLN 182

Qy 186 ISQ-----HGSDMQVDFDHAPHNFGFRFFLHYKLHKGEPFKKTCQEQTT 232
Db 183 ISQHGSDMQVDFDHAPHNFGFRFFLHYKLHKGEPFKKTCQEQTT 242

Qy 233 ETTSCLLQNVSPGDIYIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
Db 243 EMTSCLLQNVSPGDIYIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302

Qy 293 ATLFTVMCRKQKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHNV 352
Db 303 ATLFTVMCRKQKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHNV 362

Qy 353 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKHESQFIIVVCSKGMKVFVDKK 412
Db 363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKHESQFIIVVCSKGMKVFVDKK 422

Qy 413 NYKHGGGRGSGKGEFLVAVSAEKLRAQKSSAALSKEFIAYFYDYSCEGDVPGILD 472
Db 423 NYKHGGGRGSGKGEFLVAVSAEKLRAQKSSAALSKEFIAYFYDYSCEGDVPGILD 482

Qy 473 LSTKYRLMDNLPQLCSHLHSDHGLQEPQHTROGSRNRYFRSKSGRSLYVAICNMHQFI 532
Db 483 LSTKYRLMDNLPQLCSHLHSDHGLQEPQHTROGSRNRYFRSKSGRSLYVAICNMHQFI 542

Qy 533 DEEDPWFEKQVFPFHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 592
Db 543 DEEDPWFEKQVFPFHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 602

Qy 593 GPADSQHSQHGGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMPRDSGIYDSSVPSSE 652

Db	603	GPADSQHESQHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSSE	662
Qy	653	LSLPIMEGLSTDQETSSLTESVSSSSGIGEEPPALPSKLLSSGCKADLGCRSYTDEL	712
Db	663	LSLPIMEGLSTDQETSSLTESVSSSSGIGEEPPALPSKLLSSGCKADLGCRSYTDEL	722
Qy	713	HAVAPL	718
Db	723	HAVAPL	728

Search completed: August 9, 2005, 11:54:41
Job time : 106.966 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:37:17 ; Search time 28.7981 Seconds
(without alignments)
2398.896 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGRWKAARPLCVAN.....CKADLGCRSYDELHVAAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3005	78.5	564	T42695	hypothetical prote
2	170.5	4.5	846	T27282	hypothetical prote
3	126.5	3.3	718	T30113	hypothetical prote
4	117	3.1	757	T09081	telomere-associate
5	116.5	3.0	901	T83781	transposase (08) /
6	110	2.9	535	T17212	hypothetical prote
7	110	2.9	592	T19239	vesicle transport
8	110	2.9	917	T04661	hypothetical prote
9	109	2.8	998	T37627	protein-tyrosine k
10	107.5	2.8	938	T149071	protein kinase - m
11	107.5	2.8	3788	T13960	beige protein homo
12	107.5	2.8	3942	T42730	Basoon protein -
13	106.5	2.8	638	D86477	protein F1504.27 [
14	106	2.8	3788	T30851	lysosomal traffick
15	105	2.7	901	TJ6093	dead ringer nuclea
16	105	2.7	1571	T14155	zinc finger protei
17	104	2.7	1462	B36182	protein-tyrosine-p
18	103.5	2.7	663	A39897	GTPase-activating
19	103.5	2.7	930	A84668	Argonaute (AGO1)-l
20	102	2.7	813	B47485	ABR protein 2 - hu
21	102	2.7	859	A49307	98K GTPase-activat
22	102	2.7	1448	A12007	Subtilase family p
23	101.5	2.7	822	A47485	ABR protein 1 - hu
24	101.5	2.7	1639	T50119	probable sensory t
25	101	2.6	641	T05497	hypothetical prote
26	101	2.6	664	T51247	ARR2 protein limpo
27	101	2.6	1275	A38985	nucleotide exchang
28	100.5	2.6	1007	T24643	hypothetical prote
29	99.5	2.6	657	E96949	serine/threonine p

ALIGNMENTS

RESULT 1

T42695

hypothetical protein DKFZp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42695

R:Blöcker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: Z22230

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 >AAA>

A:Cross-references: UNIPROT:Q9UFA0; EMBL:AL133097

A:Experimental source: adult testis; clone DKFZp434N1928

C:Genetics:

A:Note: DKFZp434N1928.1

Query Match 78.5%; Score 3005; DB 2; Length 564;

Best Local Similarity 99.8%; Pred. No. 2.7e-232; Mismatches 1; Indels 0; Gaps 0;

Matches 563; Conservative 0;

Qy	155	HPFFRTRACDLLLQPDNLACKPFWKPRNLNLSQHGSDMQVSDHAPHNFGFRFFYLHYK	214
Db	1	HPFFRTRACDLLLQPDNLACKPFWKPRNLNLSQHGSDMQVSDHAPHNFGFRFFYLHYK	60
Qy	215	LKHEGPFKRKCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA	274
Db	61	LKHEGPFKRKCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA	120
Qy	275	GPIRAVAITVPLVVISAFATLFTWCRKKQENIYSHLDESSSESTYTAALPRRLRPR	334
Db	121	GPIRAVAITVPLVVISAFATLFTWCRKKQENIYSHLDESSSESTYTAALPRRLRPR	180
Qy	335	PKVFLCYSSKDGQNHNVVQCFAVFLQDFCCGEVALDLWEDFSLCREGREWVIQKHES	394
Db	181	PKVFLCYSSKDGQNHNVVQCFAVFLQDFCCGEVALDLWEDFSLCREGREWVIQKHES	240
Qy	395	QFIIVVCSKGMKYFVDKQYKHKGGRSGKGELFLVAVSAIAEKLRAKQSSSAALSKF	454
Db	241	QFIIVVCSKGMKYFVDKQYKHKGGRSGKGELFLVAVSAIAEKLRAKQSSSAALSKF	300
Qy	455	IATVFDYSCEGDPGILDLSTKYRLMDNLPCSLHLHRDGLQPGQHTRGSRNRYPR	514
Db	301	IATVFDYSCEGDPGILDLSTKYRLMDNLPCSLHLHRDGLQPGQHTRGSRNRYPR	360
Qy	515	SKSGRLVATCNMHQFIDIEPDMFEKQFVFPHPPLAYRFPVLEKFSGLVNDVMCKP	574
Db	361	SKSGRLVATCNMHQFIDIEPDMFEKQFVFPHPPLAYRFPVLEKFSGLVNDVMCKP	420
Qy	575	GPESDFCLKVEAAVLGATGPADSQHSQHGGLDQDGEARPALDGSAAALQPLLHTVAGSP	634

A;Reference number: Z16557; MUID:98198830; PMID:9539423
A;Accession: T09081
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-757 <SAN>
A;Cross-references: UNIPROT:O13399; EMBL:AF030885; NID:g2642221; PID:g2642222
A;Experimental source: strain FB2
C;Genetics:
A;Gene: UTASrecQ
C;Keywords: DNA binding

Query Match 3.1%; Score 117; DB 2; Length 757;
Best Local Similarity 20.4%; Pred. No. 0.6;
Matches 111; Conservative

Qy 233 ETTSCILQNVSPGDIYIELVDVDTYTKVMHYALKVHSPWAGPIRAV-----AIVPL-- 286
Db 77 ETTILPTVALRANMLAKLDVNM-----IRYVWQP-GSKKAAPILVSTEAALITLAPKE 131
Qy 287 -----VVISAFATLFTVMCKKQOENIYSHLDESESESTYTAALP----- 327
Db 132 YANRLQOORLDRIVIDECHLTITARSYRSMMQLAWHRVDVETQVWLATLPIPEDA 191
Qy 328 --RERLRPRKVP-----LYSSKDGQNMVNVQCF-AFYLODFCGCEVALDWMEDF 376
Db 192 FISHNKLTKPLIVRESTNRSLCYSVRTAEHRMSGMTCYDAVRVD--ECRARTDIW-- 246
Qy 377 SLCREGQREWIQIHESQFIIVVCSKGMKYFVDK-----KNYKHGGGSGS----- 423
Db 247 ----NGQD-----RIIVYCTS--KELVARLAEMLCGAAYSESSEADKAALIQ 290
Qy 424 ----GKELPLVAVSAITAEKLRQAKQSSAALSXFIAYFYSCGQVPGIL--DLSTKY 477
Db 291 DWICGKSPVIVATSA-----LGVFDYPHVRFVHLLGPDLLTDF 331
Qy 478 -----RLMDNLPOI-CSHLSRDHGLQFPQGHOTRQGRNRNFRS 515
Db 332 SQESGRAGDGPAPESILLAGPQLDDRAP-ASGRASSAEKGVAPG--ADKEAMQLYRS 387
Qy 516 KSGRSLYVAICNMQFIDEEDPWEKQFVPHPPPLRYEPVLEKFDGSLVINDVMCKPG 575
Db 388 RK-----YCLRGVLSQLDQSDW-----RWCMEGDQLCSVC 419
Qy 576 PESDFCLKVEAVLGGATGAPDSQH--ESQHGGLDQDGEARPALDGSAAALPLLHTVKAG 632
Db 420 PGHHF-----QARGGQGFHTAPAGDQSTQGRHPSMHGSS--HPSMH----- 463
Qy 633 SPSPMDPRDSGIYDSSVPSSE-LSLPLMEGLSTDQTTSSLTESVSSS--SGLGEEEP 688
Db 464 -----GSSHPSSHSGSHPSIHGSS-HPSIHGSGQHGQRRKQKQPD 510
Qy 689 LPSK 692
Db 511 PFSE 514

RESULT 5
F83781
transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus ha
A;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F83781
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83781
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-901 <STO>
A;Cross-references: UNIPROT:Q9BE04; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA8047
A;Experimental source: strain C-125
C;Genetics:

A;Gene: BH1054

Query Match 3.0%; Score 116.5; DB 2; Length 901;
Best Local Similarity 19.6%; Pred. No. 0.85;
Matches 112; Conservative

Qy 26 ASRNSGLYNTFKYDNCCTTVLNPVGHVIAQAQNIITISQY-ACHDQVAVTILMSPGALGI 84
Db 333 ALKESGL-----PLPKTLIADAGYSGSESNTVYMADELFFETLIPS----- 371
Qy 85 EFLKPRVILEELKSEGR-----OCQOL--ILKDPKQLNSFKRTGMESQFLNMKF 134
Db 372 ----HTFR--OEQRKSPAKKFFHPYNWRCDEDDVYWCNQRKVSFKYTKTDPY---GY 423
Qy 135 ETDYFV-----KVVPF-PSI-----KNESNYHPFFPFRTRACDILLLOPDNLACPFWKP 182
Db 424 ARDFKVVCESECGCPFPKCTKARGNRQVHNPVY-----EELKAKHQHKLK 471
Qy 183 NLNISQHG-----SDMQVSDHAPHNFGFRFFYLHYKLHKGEPFKRCKTQEQTTET 234
Db 472 ----SEEGRTLYQKRTDVSFVGHVKNLGRRLHLRGK----- 507
Qy 235 TSCLLQNVSPGDIYIELVDVDTITRKVMHYALKVHSPWAGPIRAVAITVPLVVIS-AFA 293
Db 508 -----ESVHELGLVALAHNL 524
Qy 294 TLFTVMCRKQOENIYSHLDESESESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNV 353
Db 525 KRATVDRSRKEPKNTQHNREN-----RIKRF-----SRFVVL 558
Qy 354 OCF---AYFLQDFCGCEVALDWMEDFSLCREGQREWV-----IQIHESQFIIVVCSKGMK 406
Db 559 RCFWDSPPFIKSDGQVASFALFD--KLRRREGGENMIEVIDLSKTYRNQV---KGIN 612
Qy 407 YFVDKKNYKHKGGRSGSGKGLFLVAVSAI-----AEKLRQAKQSSAALS 453
Db 613 MFTEKGMVGLLGNAGAGKSTTSMISLIQPTSGDVLIKGSHKSKAIRSILGVVPO 672
Qy 454 FIAYFYSCB-----GDVPGILDSTKYRLMDNLPLQCLSHLSRDHGLQEPQGHOTRQ 507
Db 673 EIAYVHDLTARENLAFFGKIYGLAGEELKHR-MESTLQLV-----GLEE-----RQN 718
Qy 508 SRRNYFSKSGRSLYVAICNMHQ---FIDEEP 536
Db 719 DRVHTFGGKMRRLNIAVALHHEPELLIMDEP 750

RESULT 6
TI17212
hypothetical protein DKFZp434P211.1 - human (fragments)
A;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: TI17212
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18723
A;Accession: TI17212
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-488;489-535 <POU>
A;Cross-references: UNIPROT:Q9NTU6; EMBL:AL117401
A;Experimental source: adult testis; clone DKFZp434P211
A;Note: the cDNA sequence contains a -1 frameshift near codon 488
C;Genetics:
A;Note: DKFZp434P211.1

Query Match 2.9%; Score 110; DB 2; Length 535;
Best Local Similarity 23.5%; Pred. No. 1.3;
Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

Qy 439 KLRQAKQSS-SAALSXFIATVFDVSCGDVPGI-----LDLSKYRLMDNLPO 485
Db 103 RYNQTSQTSWTSSCTNRNAISSSYSTGGLPGLKRRRGFPASSHCQLTSSSKTVSEDRPQ 162


```
Db 747 IFSTANPWNVNREINTITRVEDEELDDIDDHHPNQOQKEKQGLSGL 806
Qy 566 -----VLNDVMCKPESDFCLKVEAAVLGATGPADSHQESQHGL-----DQ 608
Db 807 SKQKMAARFNSFKGLKQMAAKNEKSVV-----TNDEKHEEKNGATVQIKKKYFTSSDE 862
Qy 609 DGEARPALDGSAAQLPLLHTVKAGSPSDMPRDSGIIYDSSVPSSELSPLMEGLGTDQDET 668
Db 863 MGAAKMA-----QSKLQD-----NLKKLGISLRITEM 890
Qy 669 SSLTESVSSSS 679
Db 891 EDTAKSFSSSTA 901

RESULT 9
S37627
protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37627
R:Boehm, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Streibhardt, K.; Ruebs
Oncogene 8, 2857-2862, 1993
A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.
A:Reference number: S37627; MUID:93390963; PMID:8397371
A:Accession: S37627
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-998 <BO>
A:Cross-references: UNIPROT:P54753; EMBL:X75208; NID:G406867; PIDN:CAA53021.1; PID:G4068
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki
F:631-899/Domain: protein kinase homology <KIN>
F:639-647/Region: protein kinase ATP-binding motif
F:922-988/Domain: SAM homology <SAM>

Query Match 2.8%; Score 109; DB 2; Length 998;
Best Local Similarity 18.9%; Pred. No. 3.9; Mismatches 301; Indels 250; Gaps 42;
Matches 157; Conservative 122;

Qy 1 ADTCGRMKAAARPLC-----VANEGVGPA-----SRNSG-----LYNITPKY 39
Db 268 ACTCATGHEPAKESQCRPCPPGSYKAKQGGPCPCPNSTRTTSPAASICTCHNNFYRA 327
Qy 40 DN-----CTTLNPVGKHVIADAQNTITISQYACHDQVAVTILWS-PGALGIEFLKGRPV 92
Db 328 DSDSADSACTTVPSP-PRGVISNV-----NETSLILEWSEPRDLGVRDLDLLNV 375
Qy 93 ILEELKSEG-----RQCOOLILKDPKOLNSPKRTGMESQPLNKKFETDYFVKVPPPS 147
Db 376 ICKKHGAGGASACSRCDNDNVEFVPRQLGLSEPRVHTS-----HLAHTRYTFEQAVNG 430
Qy 148 IKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISQHGSDMVQSFDPHAPNFGFR 207
Db 431 VSGKSPLPRPYAAVNITNQAPSEV-----PTLHSHSSGSLTISWAPPERPNG-- 481
Qy 208 FFYLHYLKLKHEGPF-KRKTCKQEQTTTSCLLQNVSP-GDYIIEBLVDDTNTTRKVMHYA 265
Db 482 -VILDYEMKY---PEKSEGIASVTISQKNSVQLDGLRDPARVYVQV-----RARTVAGY 532
Qy 266 -LKPVH-----SPWAGPIRAVAITVPLVVISAFATL-----FTVMCRKKQEQNIYSH 311
Db 533 QYSRPAEFTTTSERSGGAQQLQEQPLIVGSAATAGLVFVAVVIAIVCLRKQRH----- 587
Qy 312 LDEESSESTYTAALPRRLRPRKPVLCYSSKQGNHNVVOCFAFLQDFC-CGEVAL 370
Db 588 -----GSSEYTEKL-QQTIAPGMKVYIDPFTYEDPN--EAVREPAKIDVSCVKEIVI 639
Qy 371 DLWEDFSLCRGQREWVIOKHESQFIIVVCSKGMKYFVDKKNYKHGGGSGSGKGEIPL 430
Db 640 GAGEGGEVCR-----GRLKQPGREVF-- 661
```

```
Qy 431 VAVSAI-----AEKLROAKQSSAALSKEPIAVFYFDYSCGDPVPGILDLS---TKYR----- 478
Db 662 VAIKTLKVGVTORQRDFLSEASIMGQF-----DHPNIIIRLEGGVTKSRPVMIL 710
Qy 479 --LMDNLPOLCSHLHSDHGLQBPQHT-----RQGSRRNT-FRSKSGRS 520
Db 711 TEFMENC-ALDSFURLND-----GQFTVQLQVLMRLGIAAGMKYLSEMTVVRHDLAARN 763
Qy 521 LYV-----AIC-----NMHQFIDEEDPWFEPKQVPPFHP-----PLRYREP---VLEKFPDS 563
Db 764 ILVNSNLVKVDFGLSRFLEDDPS-----DPTYTSSLGGKIPIRWTAPEAIYARKFTS 817
Qy 564 -----GLVLDNVMCKPESDFCLKVEAAVLGATGPADSHQESQHGLDQDEARPAL 616
Db 818 ASDVMSYGIWMEVMS-----YGERPYWDMNQDVINAVEQDYRLPPEM 861
Qy 617 DGSAAQLPLLHTVKAGSPSDMPRDSGIYDS-----SVPSSELSPLMEGLS 662
Db 862 DCPTALHQLMLDCWVRDRNLRPFQSVINTLQKIRNAASLKVIASAQSGMSQPLDRTV 921
Qy 663 TDQETSSLTESVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDEL 712
Db 922 PDYTTFTVGDMLDAIK-MGRYK-----ESFVSAGFASFDLVAQMTAEDL 965

RESULT 10
149071
protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149071
R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A:Title: Identification of novel protein kinases expressed in the myocardium of the deve
A:Reference number: 149071; MUID:95200798; PMID:7893599
A:Accession: 149071
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-938 <RES>
A:Cross-references: UNIPROT:Q60669; EMBL:U11493; NID:G595418; PIDN:AAA67925.1; PID:G5954
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:571-839/Domain: protein kinase homology <KIN>
F:579-587/Region: protein kinase ATP-binding motif
F:862-928/Domain: SAM homology <SAM>

Query Match 2.8%; Score 107.5; DB 2; Length 938;
Best Local Similarity 19.3%; Pred. No. 4.7;
Matches 152; Conservative 115; Mismatches 271; Indels 251; Gaps 42;

Qy 1 ADTCGRMKAAARPLC-----VANEGVGPA-----SRNSG-----LYNITPKY 39
Db 205 ACTCATGHEPAKESQCRPCPPGSYKAKQGGPCPCPNSTRTTSPAASICTCHNNFYRA 264
Qy 40 DN-----CTTLNPVGKHVIADAQNTITISQYACHDQVAVTILWS-PGALGIEFLKGRPV 92
Db 265 DSDSADSACTTTRSP-PRGVISNV-----NETSLILEWSEPRDLGGRDLDLLNV 312
Qy 93 ILEELK-SEG-----RQCOOLILKDPKOLNSPKRTGMESQPLNKKFETDYFVKVVP 144
Db 313 ICKKRGSSGAGGPATCSRCDNDNVEFVPRQLGLTERRVHIS-----HLAHTRYTFEQVA 367
Qy 145 FPSIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISQHGSDMVQSFDPHAPNPF 204
Db 368 VNGVSGKSPLPRPYAAVNITNQAPSEV-----PTLHSHSTSGSLTISWAPPERPN 420
Qy 205 GFRFFYLHYLKLKHEGPF-KRKTCKQEQTTTSCLLQNVSP-GDYIIEBLVDDTNTTRKY- 261
Db 421 G---VILDYEMKY---FEKSKAIASVTISQKNSVQLDGLQDPARVYVQV-----RARTVA 469
Qy 262 -----MHYALKEVHPWAGPIRAVAITVPLVVISAFSA-----TLFTVMCRKKQEQNI 308
Db 470 GYGQYTHPAEFTTTSERSGGAQQLQEQPLIVGSAATAGLVFVAVVIAIVCLRKQRH-- 527
```


Query Match	2.8%;	Score 106.5;	DB 2;	Length 638;
Best Local Similarity	19.4%;	Pred. No. 3.2;		
Matches	94;	Conservative 63;	Mismatches 175;	Indels 153; Gaps 24;
Qy	59	NIITISQACHDQAVATILNSFGALGTIEFLKGFVILIELKSEGRQCOQLILKPKQLNNS	118	
Db	275	DIKYQVYSCHLQDCFYVHVS-----KCATHENVMDGKELEWIESDETEDISP	322	
Qy	119	FKRTGMESQFLNWKFTEDYFVKVPPPP---SIKNESNYHPFFFRACDALLQPDNLAC	175	
Db	323	FRNLG-----DGFIRKHFCHKRLKLNHDGARDTEKQCRAC---IYP---IVS	364	
Qy	176	KPWKPNLNIISQHG--SDMQVSDHAPHNFGFRFFYLHVYKLKHEG--FKRKTCKQEQT	231	
Db	365	HQFYHCKKCNYSLHEVCAGLSRKLDDHALN-----HTLILSPSPGKCCSACSREST	416	
Qy	232	TETTSCLLQNVSPGDYIIELVDDTNTTRKVMYHALKPVHSPWAGPIRAVAITVPLVVISA	291	
Db	417	GFSYIC--SNKGOODFVLDV-----RCISVLEVFIIHRSEH-----PISTIS	457	
Qy	292	FATLFTVMCRKKQOENIYSHLDESSE--SSTYTAA--LPRE---RLRPRPKVFLCYSSKDG	346	
Db	458	YNSKDEILCKVKCKRCIGALHQLCTICEFTWCYSCAIIIPDEIHVKFKDHPILTSCGSAD-	516	
Qy	347	QNHMNVVQCFAFYFLQDPCGCEVALDWEDFSCLREGQREWVIQKIHBESQFIIVVCSKGMK	406	
Db	517	-----NTWVCEV-----CEKQLDPKEWFTYCNK-----CCITIHH-----LHCIFGSS	553	
Qy	407	YFVDKKNYKHKGGRGSGKGELFLVAVSAIAEKLRAQKSSSAALSXFIAVFDYSCGD	466	

Db 554 VFM-----KPG-----SIPEDYGVKQV 570
 Qy 467 VPGILDISTYRLMDNIPQLCSHLHSRDHGLQEPQHTRQGSRRN--YFRSKSGRSLSY-V 523
 Db 571 V-----FRNSNTRQLCYMCHNRCITGL-----IFYEGYRRNATYYNHSNRSTRM 616
 Qy 524 AICNM 528
 Db 617 IFCSL 621
 RESULT 14
 T30851
 lysosomal trafficking regulator, long splice form - mouse
 N;Alternate names: beige protein homolog
 C;Species: Mus musculus (house mouse)
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T30851
 R;Barbosa, M.D.F.S.; Tchernev, V.T.; Kingmore, S.F.
 submitted to the EMBL Data Library, September 1996
 A;Description: Two bg or not two bg? Longest isoform of mouse *lyst* (beige) gene.
 A;Reference number: Z20903
 A;Accession: T30851
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-3788 <BAR>
 A;Cross-references: UNIPROT:P97412; EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AAC530
 A;Experimental source: strain C57BL/6J
 C;Genetics:
 A;Gene: *lyst*
 A;Map position: 1
 C;Keywords: alternative splicing
 Query Match 2.8%; Score 106; DB 2; Length 3788;
 Best Local Similarity 19.6%; Pred. No. 49;
 Matches 154; Conservative 99; Mismatches 275; Indels 256; Gaps 44;
 Qy 16 LCVANEGVGPAS-----RNSGLYNITFKYDNCITYLNPVGKVIADAQNITI 62
 Db 658 LC-----GAGPTSGLPSPSYRFQGIPLSSGSEDLMLKWDALAYQSFVQB--DRLHNIQI 711
 Qy 63 SQYACH--DQVAVITLSPGALGIEFLKGFVILELKSEG----RQCQQLIKDPPQLN 116
 Db 712 ANHICNLLOKGNVVQW-----KLYNIFNPVLOGVELVHHCQQLSPS----- 756
 Qy 117 SSPKRTGMESPFLLNMKPEF--DYFKVWP-----FPSIKN-----ESNY----- 154
 Db 757 ---AQTHMCSQLKQVLPQEVLIQYIKTLPVLKSRVIRDLFLSCNGVNHIIELNYLDGIR 813
 Qy 155 -HPF-FPRTRACDLLLOPDNIACKPFWKPRNINISOHSDMQVSPFDHAPHNFGFRFFYLH 212
 Db 814 SHSLKAFETLIVSLGEQKDAAVLDV---DGLDIQQLPSPSLV----- 853
 Qy 213 YKLXHGPPFKTKQEQETTTSCLLQNVSPGDIIELVDDTNTTRKVMHYALKPVHSP 272
 Db 854 -----GFSLHK-----QOASDSPCSLRK-----FYASLRPPDKKRTKH---QDVH-- 893
 Qy 273 WAGPIRAVAITVPLVVIISAFATLFTVMCRKKQOENITYSHLDESSSESTYTAALPRELR 332
 Db 894 -----INTINFLCVAF-----LCVSKADS-----DRESANESEDTSGYDSPSE 934
 Qy 333 PRPKVFLCYSKDGNHNVV-----QCFAIFLQDFCGCEVALDLWEDFSLCREQREWV- 387
 Db 935 PLSHMLPCLSLD-----VVLPSPECLHH-----AADIW---SMCR-----WIY 970
 Qy 388 -IQIHESQFI-----IVVCSKGMKYFVDKKNYKHGGGRSGKGELF-----LVAVSAI 436
 Db 971 MLNSVFOQFRLGGFQVCHL-LIFMI IQKLFPSHTEDQGRQGEMSRNQELIRIS-- 1027
 Qy 437 AEKLRAQKSSAALS KFIATVFDYSCSDGVPGL--DLSTKYRLMDN-----LPQ 485
 Db 1028 -----YPELTLKGDVSSATAPDLGLFLKSDSVRGFQSPVLPT 1066

Qy 486 LCSHLRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFIDEERPDWFEKQFVP 545
Db 1067 SAEQIVATE---SVPGE-----RKAFMSQOSETLSQIRLLESLLD-----IC 1106
Qy 546 FHPPPLRYRPREVLEKFDGLVNDVMCK-----PPESDFCLKVEAAVLG 590
Db 1107 LHSARACQKWELELPQGLSVENITCELREHLSQSKVAETELAKPLFDALLRVALGNHS 1166
Qy 591 A-TGPADS-----QHESQHGGLDQGEARPALDGSAAQLPLHTVKAGSPDM---PRDSG 642
Db 1167 ADLGFDAVTEKSHPSSEBLLSQPCDFSEAEADSQCCSLKLLGEEGYEADSESNPEDVD 1226
Qy 643 IYDSVPSSELSLPLMEGLSTDQTFETSSLTESVSSSGLGE---EPPALPSKLLSSGSC 699
Db 1227 TODDGV---ELN-PEAEGFS-GSIVSNLLENLTH---GEIYYEICMLGLNLLLSAKA 1277
Qy 700 KADL 703
Db 1278 KLDV 1281
RESULT 15
JC6093
dead ringer nuclear protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: JC6093
Mol. Cell. Biol. 16, 792-799, 1996
A;Title: Characterization of the dead ringer gene identifies a novel, highly conserved f
A;Reference number: JC6093; MUID:96182081; PMID:8622680
A;Accession: JC6093
A;Molecule type: mRNA
A;Residues: 1-301 <GRE>
A;Cross-references: UNIPROT:Q24573; GB:U62542; NID:g1480739; PIDN:AAB05771.1; PID:g14807
A;Experimental source: embryo
C;Genetics:
A;Gene: dri
C;Keywords: DNA binding; embryo
Query Match 2.7%; Score 105; DB 2; Length 901;
Best Local Similarity 20.4%; Pred. No. 7,1;
Matches 96; Conservative 56; Mismatches 157; Indels 162; Gaps 23;
Qy 370 LDLWEDFSL--CREG-----OREW--VIQKHESQFI-----IVVCSKGMKYF---VDK 411
Db 313 LDLYELNVIARGLVVDVINKLWQEIIGKHLPSITSAAFTLRTQYMKLYPYCEK 372
Qy 412 KNYK-----HKGGRGSGKE-----LFLVAV 433
Db 373 KNLSTPAELQAIQGNREGRRSSYGQYEAMHNMQMPPISRPSLPGMQOMSPLALVTH 432
Qy 434 SAIAEKLR-QAKOSSAALSFIAYFDYSCGDPVPGILDLSITKYRLMDNLPQLC----- 487
Db 433 AAVANNQQAQAAAAAAHRLMGA---PAGQMPNLVKQEIERSMWEYL-QLIQAKKE 487
Qy 488 -----SHLHRDHGLQEPGQH-----TRQGSRRNYFRSKGR-----SL 521
Db 488 QGMPFVLGGNHPPHQQHSQQQHHQOQQQSQOQHLLQQQRQSQSPDLSKHEALSA 547
Qy 522 YVAICNMHQ-----FIDEEDWFEKQFVFPHPPL-----RYREPVLEKFD----- 562
Db 548 QVALWHYHNNNSPPGSAHTSPQOREALNLSDSPPLTNIKREREREPTPEVDQDKFV 607
Qy 563 -----SGLVNDVMCKPGPESDFCLKVE--AAVLGATGPADSQHSQHGLDQDG 610
Db 608 DQPPPAKEVSGLL-----PPGFPANFYLNPHNMAVAAGAAG---FHHPSMGHQDAAS 658
Qy 611 EARPALDGSAAQLPLHTVTKAGSPDMPRDSGIYDSSVPSSELSLPLMEG----- 660
Db 659 EGEPEDD-----YAHGEHNTTGNSSSMHDDSEFQO-----MNGHHHHQTHILD 701

Qy 661 LSTDQTFETSSLTESVSSSGLGEEPPALPSKLLSSGSCKADLGCRSYTDE 711
Db 702 KSDDSAIENSPPTTSTTTGGSGVGRHSSPVSTK--KKGAKPQSGGKDLPT 750
Search completed: August 9, 2005, 11:49:57
Job time : 31.7981 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:36:31 ; Search time 113.24 Seconds
(without alignments)
3246.847 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGRMKAAARPRLCVAN.....CKADLGRSYTDELHVAAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3735	97.5	739	2 QNFS0	Qnfs0 homo sapien
2	3731	97.4	739	2 QNFM7	Qnfm7 homo sapien
3	3708	96.8	707	2 QERV4	Qerv4 homo sapien
4	3703	96.7	728	2 Q6UW15	Q6uw15 homo sapien
5	3222.5	84.2	738	2 Q8U7L1	Q8uj11 mus musculus
6	3170	82.8	595	2 Q8N113	Q8n113 homo sapien
7	3005	78.5	564	2 Q9UFA0	Q9ufa0 homo sapien
8	2844	74.3	741	2 Q7T2L7	Q7t217 gallus gall
9	2834	74.0	697	2 Q8AV76	Q8av76 gallus gall
10	2675.5	69.9	594	2 Q8K447	Q8k447 mus musculus
11	2616.5	68.3	582	2 Q8R5J8	Q8r5j8 mus musculus
12	1950.5	50.9	745	2 Q8QHJ9	Q8qhj9 brachydanio
13	1941.5	50.7	745	2 Q8QHJ6	Q8qhj6 brachydanio
14	354	9.2	109	2 Q8HXE8	Q8hxe8 macaca fasc
15	310	8.1	866	1 I17R_HUMAN	Q8f46 homo sapien
16	306	8.0	864	1 I17R_MOUSE	Q60943 mus musculus
17	205	5.4	769	2 Q69HQ3	Q69hq3 ciona intes
18	170.5	4.5	846	2 Q9NA64	Q9na64 caenorhabdi
19	135.5	3.5	502	1 I17S_HUMAN	Q9nm6 homo sapien
20	126.5	3.3	718	1 YS02_CAEEL	Q10128 caenorhabdi
21	121	3.2	993	2 Q7PW05	Q7pw05 anopheles g
22	117.5	3.1	562	2 Q93755	Q93755 homo sapien
23	117	3.1	757	2 Q13399	Q13399 utillago ma
24	116.5	3.0	637	2 Q6AZ51	Q6az51 rattus norv
25	116.5	3.0	901	2 Q9KE04	Q9ke04 bacillus ha
26	116	3.0	4736	2 Q7YT99	Q7yt99 mytilus gal
27	115	3.0	859	1 MR1P_HUMAN	Q8nf9 homo sapien
28	113.5	3.0	617	2 Q8K4C1	Q8k4c1 mus musculus
29	113.5	3.0	1190	2 Q6H470	Q6h470 oryza sativ
30	112.5	2.9	549	2 Q93754	Q93754 homo sapien
31	112.5	2.9	783	2 Q6FJR3	Q6fjr3 candida gla

32	112.5	2.9	1685	2	Q6H969	Q6h969 homo sapien
33	112.5	2.9	1685	2	Q6ZU00	Q6zuu0 homo sapien
34	111.5	2.9	370	2	Q8N2R7	Q8n2r7 homo sapien
35	111.5	2.9	370	2	Q96KN9	Q96kn9 homo sapien
36	111.5	2.9	862	2	Q6NUK8	Q6nuk8 homo sapien
37	111	2.9	592	2	Q6CED7	Q6ced7 varrowia li
38	110.5	2.9	499	1	I17S_MOUSE	Q9jip3 mus musculus
39	110.5	2.9	805	2	Q758M4	Q758m4 ashbya goas
40	110.5	2.9	1433	2	Q6PFW1	Q6pfi1 homo sapien
41	110	2.9	428	2	Q9NTU6	Q9ntu6 homo sapien
42	110	2.9	592	1	STB3_MOUSE	Q60770 mus musculus
43	110	2.9	618	2	Q6DE54	Q6de94 xenopus lae
44	110	2.9	917	2	Q81789	Q81789 arabidopsis
45	109.5	2.9	764	2	Q6NU08	Q6nu08 xenopus lae

ALIGNMENTS

RESULT 1

ID	Q8NFS0	PRELIMINARY;	PRT;	739 AA.
AC	Q8NFS0;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	IL-17RD.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Gilbert J.M., Gorman D.M.;			
RL	Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF458087; AAM7751.1; -.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.			
DR	InterPro; IPR000157; TIR.			
SQ	SEQUENCE 739 AA; 82440 MW; 1670803DD0C0DF17 CRC64;			

Query Match 97.5%; Score 3735; DB 2; Length 739;

Best Local Similarity 97.9%; Pred. No. 7.8e-275;

Matches 703; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

Qy	1	ADTCGRMKAAARPRLCVANEGVGPASRNSGLNITFKYDNCCTTYLNPVGHVIADAQNI	60
Db	36	ADTCGRMKAAARPRLCVANEGVGPASRNSGLNITFKYDNCCTTYLNPVGHVIADAQNI	81
Qy	61	TISQYACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSFK	120
Db	82	TISQYACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSFK	141
Qy	121	RTGMESQFLNMKPTDYFVKVPFPSPISKNSNTHPPFPFRTRACDLILLOPNLACKPFWK	180
Db	142	RTGMESQFLNMKPTDYFVKVPFPSPISKNSNTHPPFPFRTRACDLILLOPNLACKPFWK	201
Qy	191	PRNLNISQSGDMQVSDPHAPNFGFRFFYLHYKLKHGPPFKRCKTQBOETTTSCLLQ	240
Db	202	PRNLNISQSGDMQVSDPHAPNFGFRFFYLHYKLKHGPPFKRCKTQBOETTTSCLLQ	261
Qy	241	NVSPGDYIIELVDDTNTTRKVMHYALKVPHSPWAGPIRAVAITVPLVVISAFATLFTVMC	300
Db	262	NVSPGDYIIELVDDTNTTRKVMHYALKVPHSPWAGPIRAVAITVPLVVISAFATLFTVMC	321
Qy	301	RKQOENYSHLDESSSSSTYTAALPRERLRPRPKVFLCYSSKQGNHNMVQCFAFPL	360
Db	322	RKQOENYSHLDESSSSSTYTAALPRERLRPRPKVFLCYSSKQGNHNMVQCFAFPL	381
Qy	361	QDFCGCEVALDLWEDFSLCRGQREWVTKTHESQFIIVVCSKGMKYFVDKKNYKHGGG	420
Db	382	QDFCGCEVALDLWEDFSLCRGQREWVTKTHESQFIIVVCSKGMKYFVDKKNYKHGGG	441

141 KVPFPSPKSNESVHPFFRTRACDLQLQDNLACKPFWKPRNLNISOHGSMDQVSPDHA 200
130 KVPFPSPKSNESVHPFFRTRACDLQLQDNLACKPFWKPRNLNISOHGSMDQVSPDHA 189
201 PHNFGFRFFLHYKLKHEGPFKRTCKOETTTSCLLQNVSPGDYIIELVDDTNTTRK 260
190 PHNFGFRFFLHYKLKHEGPFKRTCKOETTTSCLLQNVSPGDYIIELVDDTNTTRK 249
261 VMHYALKPVSHPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDEESSESS 320
250 VMHYALKPVSHPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDEESSESS 309
321 TYTAALPRERLRPRPKPVFLCVSSKDGQNMNVVOCFAYFLQDFCGCEVALDLWEDFSLCR 380
310 TYTAALPRERLRPRPKPVFLCVSSKDGQNMNVVOCFAYFLQDFCGCEVALDLWEDFSLCR 369
381 EGQREWIQKHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKL 440
370 EGQREWIQKHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKL 429
441 ROAQSSAALSKEPIAVYFDYSCGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEP 500
430 ROAQSSAALSKEPIAVYFDYSCGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEP 489
501 GOHTRQSRNNYFRSKSGRSIYVAICNMHOFIDEEPWFKEQFVPPHPPPLRYREPVLK 560
490 GOHTRQSRNNYFRSKSGRSIYVAICNMHOFIDEEPWFKEQFVPPHPPPLRYREPVLK 549
561 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGADSPADSOHESQHGGLQDGEARPALDGS 620
550 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGADSPADSOHESQHGGLQDGEARPALDGS 609
621 ALQPLHTVXAGSPDMRDSGIYDSSVPSSELSPLMEGLSTQDTTSSLTSSVSSSG 680
610 ALQPLHTVXAGSPDMRDSGIYDSSVPSSELSPLMEGLSTQDTTSSLTSSVSSSG 669
681 LGREPPALPSKLLSSGCKADLCRSYTDLHVAAPL 718
670 LGREPPALPSKLLSSGCKADLCRSYTDLHVAAPL 707

RESULT 4
Q6UW15 PRELIMINARY; PRT; 728 AA.
ID Q6UW15
AC Q6UW15;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IL17Rhom.
GN ORFNames=UNQ6115;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBITaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robb E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358774; RAQ89134.1; -
GO; GO:0016020; C:membrane; IEA.

DR GO:0004888; F:transmembrane receptor activity; IEA.
SQ InterPro; IPR00157; TIR.
SR SEQUENCE 728 AA; 81310 MW; 4AD9D3F6B1C78C26 CRC64;
Query Match 96.7%; Score 3703; DB 2; Length 728;
Best Local Similarity 96.7%; Pred. No. 2.1e-272; Indels 14; Gaps 2;
Matches 702; Conservative 2; Mismatches 8;
QY 7 RMKAARPRICVANE-GVGPASRNSGLYNTFFKYDNCCTTYLNPVGKHVIAADAQNTISQY 65
DB 3 RASASGVPAIFVSGEQGVGPASRNSGLYNTFFKYDNCCTTYLNPVGKHVIAADAQNTISQY 62
QY 66 ACHQDAVATILWSPGALGIEFLKGFVRVILBELSEGRQCOQLILKDPQLNSSFRTGME 125
DB 63 ACHQDAVATILWSPGALGIEFLKGFVRVILBELSEGRQCOQLILKDPQLNSSFRTGME 122
QY 126 SQPLNWKFTDYFVKVVPFPPSIKNESNYHFFRTRACDLQLQDNLACKPFWKPRNLN 185
DB 123 SQPLNWKFTDYFVKVVPFPPSIKNESNYHFFRTRACDLQLQDNLACKPFWKPRNLN 182
QY 186 ISQ-----HGSDMQVSFDHAPNFGFRFFLHYKLKHEGPFKRTCKQOQT 232
DB 183 ISQHGSDMQVSFDHAPNFGFRFFLHYKLKHEGPFKRTCKQOQT 242
QY 233 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 292
DB 243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 302
QY 293 ATLFTVMCRKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSKDGQNMNV 352
DB 303 ATLFTVMCRKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSKDGQNMNV 362
QY 353 VQCFAYFLQDFCGCEVALDLWEDFSLCREGOREWIOKIHESQFIIVVCSKGMKYFVDK 412
DB 363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGOREWIOKIHESQFIIVVCSKGMKYFVDK 422
QY 413 NYKHKGGRSGKGLFLVAVSAIAEKLRAQKSSAALSKEPIAVYFDYSCGDVPGILD 472
DB 423 NYKHKGGRSGKGLFLVAVSAIAEKLRAQKSSAALSKEPIAVYFDYSCGDVPGILD 482
QY 473 LSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSIYVAICNMHOFI 532
DB 483 LSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSIYVAICNMHOFI 542
QY 533 DEEPDWFKEQFVPPHPPPLRYREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAAVLGAT 592
DB 543 DEEPDWFKEQFVPPHPPPLRYREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAAVLGAT 602
QY 593 GPADSOHESQHGGLQDGEARPALDGSAAALQPLHTVXAGSPDMRDSGIYDSSVPSSE 652
DB 603 GPADSOHESQHGGLQDGEARPALDGSAAALQPLHTVXAGSPDMRDSGIYDSSVPSSE 662
QY 653 LSLPLMEGLSTQDTTSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADLCRSYTDL 712
DB 663 LSLPLMEGLSTQDTTSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADLCRSYTDL 722
QY 713 HAVAPL 718
DB 723 HAVAPL 728

RESULT 5
Q8JZL1 PRELIMINARY; PRT; 738 AA.
ID Q8JZL1
AC Q8JZL1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transmembrane protein (Interleukin 17 receptor-like protein long form).
DE Name=il17rd; Synonyms=il17rlm, Sef;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21959295; PubMed=11960706; DOI=10.1016/S0925-4773(02)00018-7;
RX Lin W., Furthauer M., Thiesse B., Thiesse C., Jing N., Ang S.-L.;
RT "Cloning of the mouse Sef gene and comparative analysis of its
RL expression with Fgf8 and Spry2 during embryogenesis.";
RL Mech. Dev. 113:163-168(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RL Liu L., Chang Z.;
RT "Sef inhibits PC-12 cell differentiation by interfering with Ras-
RL mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X.Y.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF459444; AAM28441.1; -
DR EMBL; AF494210; AAM74079.1; -
DR MGD; MGI:2159727; Il17rd.
DR DR GO; GO:0016021; C:integral to membrane; IEA.
DR DR GO; GO:0005634; C:nucleus; IEA.
DR DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR DR GO; GO:0008270; F:zinc ion binding; IEA.
DR DR InterPro; IPR000157; TIR.
DR DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
DR DR Receptor; Transmembrane.
SQ SEQUENCE 738 AA; 82347 MW; D8CE56230E3B8226 CRC64;

Query Match 84.2%; Score 3222.5; DB 2; Length 738;
Best Local Similarity 84.9%; Pred. No. 6.8e-236;
Matches 612; Conservative 37; Mismatches 51; Indels 21; Gaps 5;

Qy 1 ADTCGWRKMAAARPLCLVANEVGVPASRNSGLNITPKYDNCCTYLPVGVGHVIADAQNI 60
Db |||||
36 ADTCGR-----GVGPASRNSGLNITPKYDNCCTYLPVGGKHAIDAQNI 81
Qy 61 TISQYACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCQQLILKDPKQLNSSFX 120
Db |||||
82 TISQYACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCQQLILKDPKQLNSSFR 141
Qy 121 RTGMESQPFLLNMKPEFDYFVKVVPFPPSIKNESNHYHPPFTRACDILLQPDNLACKPFWK 180
Db |||||
142 RTGMESQPFLLNMKPEFDYFVKVVPFPPSIKNESNHYHPPFTRACDILLQPDNLACKPFWK 201
Qy 181 PRNLNISOHSDMOVSFDHAPHNFGFRFFYLHYLKHGEPFKRTCKOEQTTSCLLQ 240
Db |||||
202 PRNLNISOHSDMHVSFDHAPHNFGFRFFYLHYLKHGEPFKRTCKOEQTTSCLLQ 261
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db |||||
262 NVSPGDYIIELVDDTNTTRKAAQVYVKSQSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy 301 RKQQENIYSHLDESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVQCFAYFL 360
Db |||||
322 RKQQENIYSHLDESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVQCFAYFL 381
Qy 361 QDFCGCEVALDLWEDFSLCREGQREWAIQKHESQFIIVVCSKGMKYFVDKKNYKHGGG 420
Db |||||
382 QDFCGCEVALDLWEDFSLCREGQREWAIQKHESQFIIVVCSKGMKYFVDKKNYKHGGG 441
Qy 421 RGSKGELFLVAVSAIAEKLQAQSSAALSKEIAVYFDYSCGDDVPGIILDLSTKYRLM 480
Db |||||
442 RGAQGEFFLVAVAAIAEKLQAQSSAALRKFIIVYFDYSCGDDVPGIILDLSTKYRLM 501
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481 DNLPLQCSLHLSRDHGLQEP-GQHTRQGSRRNFRSKSGSLYVAICNMHQFIDEEPWF 539
502 DHLPELCAHLHS--GEQEVLGQHPGHSRRNFRSKSGSLYVAICNMHQFIDEEPWF 558
540 EKQVFPFPPPLRYRPPVLEKFDGSLVNDVMCKPGPESDFCLKVEAAVLGATGPADSOH 599
559 EKQFIPFQHPVRYQRPVLEKFDGSLVNDVSKPGPESDFCKRVEACVLGAAGPADSYS 618
600 --ESQHGGLDQDGEARPALDGSAAQLPLLHTVKAQSPSDMPRDSGIYDSSVPSSELSPL 657
619 YLESQHVGLDQDTEAQPSCDAPALQPLLHNAVKAQSPSEMPRDSGIYDSSVPSSELSPL 678
658 MEGLSLTDQETSSLTSSVSSSSGLGEEPPALSKLLSSGCKADLCRCGYTDELHVAAP 717
679 MEGLSLTDQETSSLTSSVSSSSGLGREDPPTLPSKLLASGVSR-EGCHSHTELOALAP 737
718 L 718
738 L 738

RESULT 6
Q8N113 PRELIMINARY; PRT; 595 AA.
AC Q8N113;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin 17 receptor-like protein short form (Hypothetical protein
DE DKFZp434L0320).
GN Name=IL17RLM; Synonyms=DKFZp434L0320;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12959313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RL Liu L., Chang Z.;
RT "Sef inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Othenwaeider B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF494211; AAM74080.1; -
DR EMBL; AL8333913; CAD38769.1; -
DR DR GO; GO:0016020; C:membrane; IEA.
DR DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR DR InterPro; IPR000157; TIR.
DR DR Hypothetical protein; Receptor.
SQ SEQUENCE 595 AA; 66846 MW; 7E6BBB64F73B2112 CRC64;

Query Match 82.8%; Score 3170; DB 2; Length 595;
Best Local Similarity 99.8%; Pred. No. 4.9e-232;
Matches 594; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 124 MESQPFLLNMKPEFDYFVKVVPFPPSIKNESNHYHPPFTRACDILLQPDNLACKPFWKPRN 183
Db |||||
1 MESQPFLLNMKPEFDYFVKVVPFPPSIKNESNHYHPPFTRACDILLQPDNLACKPFWKPRN 60
Qy 184 LNISOHSDMOVSFDHAPHNFGFRFFYLHYLKHGEPFKRTCKOEQTTSCLLQNV 243
Db |||||
61 LNISOHSDMOVSFDHAPHNFGFRFFYLHYLKHGEPFKRTCKOEQTTSCLLQNV 120
Qy 244 PGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 303
Db |||||
121 PGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 180
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QY 304 QENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKGGQNHMMNVQCFAYFLQDF 363
DB 181 QENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKGGQNHMMNVQCFAYFLQDF 240
QY 364 CGCEVALDLWDFSLCREGQREWIQKHESQFIIVVCSKGMKVFVDKKNYKHGGGRGS 423
DB 241 CGCEVALDLWDFSLCREGQREWIQKHESQFIIVVCSKGMKVFVDKKNYKHGGGRGS 300
QY 424 KGELFLVAVSAIAEKLRQAKSSAALSKEFIIVVCSKGMKVFVDKKNYKHGGGRGS 483
DB 301 KGELFLVAVSAIAEKLRQAKSSAALSKEFIIVVCSKGMKVFVDKKNYKHGGGRGS 360
QY 484 POLCSHLHSRDHGLQEPQHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQF 543
DB 361 POLCSHLHSRDHGLQEPQHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQF 420
QY 544 VPFPPLRYREPVLKFDGLVNDVMCKPGPSDFCLKVEAAVLGATGAPDSQHSQH 603
DB 421 VPFPPLRYREPVLKFDGLVNDVMCKPGPSDFCLKVEAAVLGATGAPDSQHSQH 480
QY 604 GGLDODGEARPALDGSAAALQPLHTVTKAGSPDMPDROSGIYDSSVSPSELPLMEGLST 663
DB 481 GGLDODGEARPALDGSAAALQPLHTVTKAGSPDMPDROSGIYDSSVSPSELPLMEGLST 540
QY 664 DOTETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDHHAVALP 718
DB 541 DOTETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDHHAVALP 595
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RESULT 7

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Q9UFAO PRELIMINARY; PRT; 564 AA.
ID Q9UFAO
AC Q9UFAO;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DE Hypothetical protein DKEPp434N1928 (Fragment).
GN Name=DKEPp434N1928;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133097; CAB61408.1; -
DR FIR; T42695; T42695.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523B88C CRC64;
```

Query Match 78.5%; Score 3005; DB 2; Length 564;
Best Local Similarity 99.8%; Pred. No. 1.6e-219;
Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 155 HPFFRTRACDILLQDNLACPKFWKPRNLNISOHGSMDQVSDHAPNFGFRFFVLYHK 214
DB 1 HPFFRTRACDILLQDNLACPKFWKPRNLNISOHGSMDQVSDHAPNFGFRFFVLYHK 60
QY 215 LKHEGPFKKTKQEQTTTSCLLQNVSPGYIIELVDDTNTTKVMHYALKPVHSPA 274
DB 61 LKHEGPFKKTKQEQTTTSCLLQNVSPGYIIELVDDTNTTKVMHYALKPVHSPA 120
QY 275 GPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAALPRERLR 334
DB 121 GPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAALPRERLR 180
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QY 335 PKVFLCYSSKGGQNHMMNVQCFAYFLQDFCGCEVALDLWDFSLCREGQREWIQKHES 394
DB 181 PKVFLCYSSKGGQNHMMNVQCFAYFLQDFCGCEVALDLWDFSLCREGQREWIQKHES 240
QY 395 QFIIVVCSKGMKVFVDKKNYKHGGGRSGKGEFLVAVSAIAEKLRQAKSSAALSKEF 454
DB 241 QFIIVVCSKGMKVFVDKKNYKHGGGRSGKGEFLVAVSAIAEKLRQAKSSAALSKEF 300
QY 455 IAVYFDYSCGDVPGIILDLSTKYRLMDNLPLQCSHLHSRDHGLQEPQHTROGSRNRYFR 514
DB 301 IAVYFDYSCGDVPGIILDLSTKYRLMDNLPLQCSHLHSRDHGLQEPQHTROGSRNRYFR 360
QY 515 SKGRSLYVAICNMHQFIDEEPWFKEQFVPFPPLRYREPVLKFDGLVNDVMCKP 574
DB 361 SKGRSLYVAICNMHQFIDEEPWFKEQFVPFPPLRYREPVLKFDGLVNDVMCKP 420
QY 575 GPESDFCLKVEAAVLGATGAPDSQHSQHSOGGLDODGEARPALDGSAAALQPLHTVTKAGSP 634
DB 421 GPESDFCLKVEAAVLGATGAPDSQHSQHSOGGLDODGEARPALDGSAAALQPLHTVTKAGSP 480
QY 635 SDMPRDSGIYDSSVSPSELPLMEGLSTDOTETSSLTESVSSSSGLGEEPPALPSKLL 694
DB 481 SDMPRDSGIYDSSVSPSELPLMEGLSTDOTETSSLTESVSSSSGLGEEPPALPSKLL 540
QY 695 SSGCKADLGCRSYTDHHAVALP 718
DB 541 SSGCKADLGCRSYTDHHAVALP 564
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RESULT 8

```
Q7T2L7 PRELIMINARY; PRT; 741 AA.
ID Q7T2L7
AC Q7T2L7;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DE FGF signalling antagonist SEF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22660508; PubMed=12766772; DOI=10.1038/ncb989;
RA Kawakami Y., Rodriguez-Leon J., Koth C.M., Buscher D., Itoh T.,
RA Raya A., Ng J.K., Rodriguez Esteban C., Takahashi S., Henrique D.,
RA Schwarz M.-F., Asahara H., Izpisua Belmonte J.C.;
RT "MKP3 mediates the cellular response to FGF8 signalling in the
RT vertebrate limb.";
RL Nat. Cell Biol. 5:513-519(2003).
DR EMBL; AY278204; AAP70001.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 741 AA; 83553 MW; 64B8E88241AC60CF CRC64;
```

Query Match 74.3%; Score 2844; DB 2; Length 741;
Best Local Similarity 74.0%; Pred. No. 3.9e-207;
Matches 533; Conservative 75; Mismatches 94; Indels 18; Gaps 5;

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QY 1 ADTCGWRKMAAARPLRCVANEGVGPASRNSGLYNTTFKYDNCCTYLNVPVGHVIAQAQNI 60
DB 38 ADACGR-----GLSSVTKSNGLNITTFKYDNCCTYLNVPVGHVIGDVQNI 83
QY 61 TISQACHDQAVTILWSPGALGIEFLKGFVRVILEELSEGQCQOOLIKDKPQLNSSPK 120
DB 84 TISQACHDQAVTILWSPGALGIEFLKGFVRVILEELSEGQCQOOLIKDKPQLNSSPK 143
QY 121 RTGMESQFLNMKFTDYFKVVPFPIKNSNHYHFFRTRPCDLLQPDNLACKPFWK 180
DB 144 RTGMESNPFANLKFETDYFKVVPFPIKNSNHYHFFRTRPCDLLQPDNLACKPFWK 203
```


DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0004888; F:transmembrane receptor activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Receptor.
SQ SEQUENCE 594 AA; 66780 MW; EABE6B655DCP4EC3 CRC64;

Query Match 69.9%; Score 2675.5; DB 2; Length 594;
Best Local Similarity 84.8%; Pred. No. 1.8e-194; Indels 7; Gaps 4;
Matches 507; Conservative 34; Mismatches 50;

Qy 124 MESQFLNMKPEYDFVKVVPFPPIKNEYNHPPFTRACDILLQPDNLACKPFWKPRN 183
Db 1 MESQFLNMKPEYDFVKVVPFPPIKNEYNHPPFTRACDILLQPDNLACKPFWKPRN 60

Qy 184 LNIHQSGDMQVSDHAPHNPFRRFYLYKHLKHEGPFKTKCKOQTETTSCLLNQVS 243
Db 61 LNIHQSGDMHVSFDHAPNPFRRFYLYKHLKHEGPFRRTRCRDQNTETTSCLLNQVS 120

Qy 244 PGDYIIELVDNTNTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 303
Db 121 PGDYIIELVDNSNTRKAAQVVKVSVQSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 180

Qy 304 QQENIYSHLDESSSTYTAALPRRLPRPKVFLCYSSKQGNHNVVQCPAYFLQDF 363
Db 181 QQENIYSHLDESSSTYTAALPRDLRPQPKVFLCYSKQGNHNVVQCPAYFLQDF 240

Qy 364 CGCEVALDLWDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRGS 423
Db 241 CGCEVALDLWDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRGE 300

Qy 424 KGELFLVAVSAIAEKLRQAQSSAALSKFIAYFYDSCGDPVGLDLSTKYRLMDNL 483
Db 301 AQGEFFLVAVAAIAEKLRQAQSSAALSKFIAYFYDSCGDPVGLDLSTKYRLMDHL 360

Qy 484 POLCSHLHSDHGLQEP--GQHTROGSRNNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQ 542
Db 361 PELCAHLHS-----GQEVLGQHPGHSRRNNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQ 417

Qy 543 FVPFHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATPADSQH--E 600
Db 418 FIPQHPVPRVQEPVLEKFDGLVNDVISKGPESDFCRKVEACVLGAAGPADSYSYLE 477

Qy 601 SQHGLDQDGAARPALDGSALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEG 660
Db 478 SQHVLQDQTEAQPSCDSAPALQPLLHVAVKAGSPSEMPRDSGIYDSSVPSSLSLPLMEG 537

Qy 661 LSTQDTETSSLTESVSSSGIGEEPPALPSKLLSSGCKADLGCSTYDELHVAAPL 718
Db 538 LSPQIETSLTESVSSSGIGEEPPALPSKLLFASGVSR--EHGCHSHTDLQALAPL 594

RESULT 11
Q8R5J8 PRELIMINARY; PRT; 582 AA.
AC Q8R5J8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar expression to FGF protein (Fragment).
GN Name=ll17rd; Synonyms=Seif;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21824237; PubMed=11802165; DOI=10.1038/ncb750;
RA Furthauer M., Lin W., Ang S.L., Thiese B., Thiese C.;
RT "Seif is a feedback-induced antagonist of Ras/MAPK-mediated FGF
RT signalling."

RL Nat. Cell Biol. 4:170-174 (2002).
DR EMBL; AF424804; AAL79530.1; -
DR MGD; MGI:2159727; Il17rd.
DR GO:0016020; C:membrane; IEA.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0004888; F:transmembrane receptor activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
FT NON TER 1
SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 68.3%; Score 2616.5; DB 2; Length 582;
Best Local Similarity 84.6%; Pred. No. 5.4e-130;
Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;

Qy 136 TDYFVKVVPFPPIKNEYNHPPFTRACDILLQPDNLACKPFWKPRNLSHQSGDMQV 195
Db 1 TDYFVKVVPFPPIKNEYNHPPFTRACDILLQPDNLACKPFWKPRNLSHQSGDMHV 60

Qy 196 SFDHAPHNPFRRFYLYKHLKHEGPFKTKCKOQTETTSCLLNQVSPGYIIELVDNT 255
Db 61 SFDHAPHNPFRRFYLYKHLKHEGPFRRTRCRDQNTETTSCLLNQVSPGYIIELVDNS 120

Qy 256 NTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEE 315
Db 121 NTRKAAQVVKVSVQSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEE 180

Qy 316 SSESSTYTAALPRRLPRPKVFLCYSSKQGNHNVVQCPAYFLQDFCGCEVALDLWED 375
Db 181 SPESSTYTAALPRDLRPQPKVFLCYSKQGNHNVVQCPAYFLQDFCGCEVALDLWED 240

Qy 376 FSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRSGKGLFLVAVSA 435
Db 241 FSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRSGKGLFLVAVAA 300

Qy 436 IAEKLRQAQSSAALSKFIAYFYDSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDH 495
Db 301 IAEKLRQAQSSAALSKFIAYFYDSCGDPVGLDLSTKYRLMDHLPELCAHLHS--- 357

Qy 496 GLQEP--GQHTROGSRNNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQFVFPHPPLRY 554
Db 358 GEQEVLGQHPGHSRRNNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQFIPOHPPVRYQ 417

Qy 555 EPVLEKFDGLVNDVMCKPGPESDFCLKVEAAVLGATPADSQH--ESQHGGLDQDGEA 612
Db 418 EPVLEKFDGLVNDVISKGPESDFCRKVEACVLGAAGPADSYSYLESHVGLDQDTEA 477

Qy 613 RPAIDGSAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDQETSSLT 672
Db 478 QPSCDSAPALQPLLHVAVKAGSPSEMPRDSGIYDSSVPSSLSLPLMEGLSTDQETSSLT 537

Qy 673 ESVSSSGIGEEPPALPSKLLSSGCKADLGCSTYDELHVAAPL 718
Db 538 ESVSSSGIGEEPPALPSKLLASGVSR--EHGCHSHTDLQALAPL 582

RESULT 12
Q8QHJ9 PRELIMINARY; PRT; 745 AA.
AC Q8QHJ9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Seif.
GN Name=ll17rd; Synonyms=seif; (Danio rerio).
OS Brachydanio rerio (Zebrafish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

[illegible]


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Db      100  LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDOE 156
Qy      138  YFVKV--VPPPSIKNESNYHPFFRTRACDLLLPDNLAK---PFWKPRNL----- 184
Db      157  YEVTVHLPKPPIPDGDPNHQSKNLFVDPDCEHARMKVTPCMSSGSLWDP-NITVETLEAH 215
Qy      185  -----NISQSGDMQVSFDHAPHNFGFRFPFYLHYLKHGPFKPKCKQEQTTETT 235
Db      216  QLRVSFTLWNESTHYQILLTSFPMENHSCFEHMH-HIPAPRPEEFHQRSNVTLTLNLK 274
Qy      236  SCLLQNVSPGDYIITELVDDT---NTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAF 292
Db      275  GCCRHQVQIQPFSSCLNCLRHSAVSCPEMPDTPPIPDYMLWVYWFITGISILLVG 334
Qy      293  ATLETVMCRKKQQENIYSHLDESSSESTYTAALPRERLRPRP-----KVFLCYSSKDGQN 348
Db      335  SVILLIVMTWRLAGPGS--EKYSDDTKYTDGLPVADLIPPLKPRKWIYSA-DHPL 390
Qy      349  HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREQREWV---IQKHESQFIIVVCSKG 404
Db      391  YVDVVLKPAQFLTACGTEVALDLLEEQAISEAGVMTWVGROKQEMVESNKIIVLCERG 450
Qy      405  MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLROAKQSSAALSXFIA 456
Db      451  TR-----AKWQALLGRGAPVRLRCDHGKPVGDLFTAANNMILPDFKR-----PACFGTYVV 501
Qy      457  VYF-DYSCGEGVPGILDSTKYRLMDNLPQLCSHLHSRDHGLQBPQHTROG--SRNRYF 513
Db      502  CYFSEVSCDGDVDPDLFGAAPRYPLMDRFEEV--YFRIQDLEMFPQGRMHRVGLSGDNYL 559
Qy      514  RSKSGRSIYVAICNMHQFIDEEDWFE-----KQFVPPHPPPLYREBPVLEKFDGSL 565
Db      560  RSPGGRQLRAALDRFDWQVHCDFWFCENLYSADDQDAPSLDEEV-FEBPLLP-GTGI 617
Qy      566  VLNDVMCKGPESDFCLKVEAAVLGATGPADSOHE-----SQHGG 605
Db      618  VKRAPLVRE-PGSOACLAIDPLVGEEGAIVAKLEPHLQPRGQAPQPLHTLVLAEEGA 676
Qy      606  LDQDGEARPALDGA---ALQ-----PLHTVKGSPSDMRDSGIYDSSVPSSLSLP 656
Db      677  LVAAVEPGPLADGAAVRLALAGEGEACFLLGSPGAG-----RNSVLF---LPVDPEDSP 727
Qy      657  LMEGLSTDQTTETSTLTSVSSSGLGREEPPALPSKLLSSGCKADLGC 705
Db      728  L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768
```

Search completed: August 9, 2005, 11:48:54
Job time : 117.24 secs